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               protein search, using sw model
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88
1 CECNIKVKDVNDNF
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Human-11 cadherin p
Rat-411 cadherin p
Rat-551 cadherin p
Rat-314 cadherin p
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Rat-224 cadherin p
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Self epitope of de
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D 12-SEP-1996.

D 12-SEP-1996; U03182.

F 07-MAR-1995; U03-400796.

R 07-MAR-1995; U03-400796.

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A (HARD) HARVARD COLLEGE.

I Strominger JL, Wucherpfennig KW:

I Strominger JL, Wucherpfennig KW:

Pemphigus vulgaris auto-antigens and multiple sclerosis non-self pemphigus vulgaris auto-antigens treatment, and method for antigens - useful in disease treatment, and method for auto-immune disease

I dentification of other self and non-self antigens implicated in auto-immune disease

Claim 1: Page 40: 58pp: English.

Charmaceutical preparations for tolerisation to antigens comprise
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                  18-FEB-1997 (first entry)
Self epitope of desmoglein 3, implicated in autoimmune disease.
Tolerisation; self-epitope; antigen; autoimmune disease;
autoantigen; HIA; human leukocyte antigen; T-cell; thymocyte;
pemphigus vulgaris; desmoglein; multiple sclerosis;
herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
influenza; haemagglutinin; reovirus; sigma protein.
                                                                                                                                                                                                                                         Homo sapiens.
WO9627387-A1.
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18-FEB-1997
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l Similarity 100
15; Conservative
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Pred. No. 1.7
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Gaps	ngth 999; Indels 0;	B 1; Le 7e-06; 0;	; Score 88; D ; Pred. No. 1. 0; Mismatches	100.0%; 100.0%; tive	h 100 Similarity 100 15; Conservative	Matc Local	Query Best Match	
et offi	proteins for n. The protein d treatment of	- useful in 130kD antige diagnosis an	118. 198918. 198918. 198918. 198019 VIDAN SERVICE. 198019 VIDAN STANLEY JR. 198019 VIDAN STANLEY JR. 198019 VIDAN STANLEY JR. 198019 VIDAN SERVICE. 198019	Il8. TH & HU THUN V, run V, pentic opertic operphi may be It is t	-A. 91; 798918. 91; US-798918. 91; US-798918. 8 DEPT HEALTH & H KLAUS-KOVTUN V, 167435/08. 135992. 135992. 15 and therapeutic 16 and therapeutic 16 and therapeutic 17; 50pp; E 18; F1g 7; 50pp; E 19; F1g 7; F	38918- 307-199 307-199 307-199 31 M, 31 M, 31 M, 31 M, 31 M, 31 M, 31 M, 31 M, 31 M, 32 M, 33 M, 34 M, 35 M, 36 M, 37 M, 38		
	adhesion.	tigen. autoantibodies; glycoprotein; cell	** <u></u>	Protein; 9 st entry) ulgaris 13 s; skin di surface a	standard; Pro 1993 (first 1993 vulgaris; ocyte cell su piens.	1 30742; 30742; 4-JUN- uman p emphig eratin omo sa	RESULT R30742 ID R AC R DT 1 DE H CRW P KW P CS H	
herin-6. f alterna f ccadheri vely spli tocadheri cocadheri	Human cadherin-6. Product of alterna Human protocadheri Alternatively spli Human protocadhari Protocadherin clon	STNS	R43564 R58911 R58906 R87152 R86866 R87146	391 1 1203 1 1026 1 1203 1 1203 1 797 1 1026 1	5555555 50000 00000	44444	444 410 444 45	

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Matches 15
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH) NISHUKAWA T.
(NISH) NISHUKAWA T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgGl hinge region and the resulting fusion protein is useful to treat or diagnose
                  17-JUN-1997 (first entry)
Pemphigus foliaceus antigen-IgG constant region fusion protein.
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection; ss.
                                                                                                                                                                         W15489 standard;
W15489;
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J08188540-A.
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Pemphigus vulgaris antigen protein extracellular region.
Pemphigus vulgaris antigen protein extracellular region.
Autoantibody: immunoglobulin G; IgGl; fusion protein; diagnosis;
Autoantibody: immunoglobulin G; IgGl; bulla; blister; skin disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pemphigus vulgaris.
Sequence 614 AA;
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Pred. No. 1.66
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PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pr pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell adhesion and regulation activities pc5 - involved in cell-cell scale of the protocadherins. This cc sequence represents the human protocadherin pc3. These sequences are crelated to cadherin, and possess cell adhesive ability. Cadherins are composed of an N-terminal extracellular domain cadhesion. Cadherins are composed of an N-terminal extracellular domain consists of 5 unique subdomains, a membrane spanning domain, and a c-terminal cytoplasmic domain. The cytoplasmic domain interacts with the cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. The sequences were isolated using primers I and 2 (see T03575 and consisted properties. Antibodies produced against these sequences are useful for modulating the binding activity of these cc protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propendition foliaceus antigen-IgG constant region fusion protein - linked protein 1: Page 10-12; 17pp; Japanese.

Claim 1: Page 10-12; 17pp; Japanese.

CThis sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar ct dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is cspecially administered through an adsorbent upon which the fusion protein is immobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful in immunodiagnosis. The fusion protein has little or no side effects. Sequence 778 AA;
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26-JUN-1995; UO8071.
27-JUN-1994; US-268161.
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WO9600289-A1.
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P-PSDB; T66428
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domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catenin; therapy.
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R86865;
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WPI; 97-241758/22.
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12-SEP-1995;
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12; Conserv
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1. .545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pc3.
pc4; pc5; human; rat; cadherin; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787
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Pred. No. 0.00025;
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RESULT
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Best Local
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Best Local Similarity

Matches 9; Conser
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15-MAY-1997; US-046595.
(CYTO-) CYTOGEN CORP.
(ELAN-) ELAN CORP PLC.
Alvarez VL. Belinka BA, Cag
Omahony DJ, Patterson CA, S
R58865;
                                                                                                                                                                                                                                                                                                                                                                                                                                            through, the gastrointestinal tract, e.g. insulin or leuprolide Disclosure; Fig 2; 294pp; English.

This sequence is the human HPT-1 protein. The invention relates to purified proteins (I) that bind specifically to at least one of th gastro-intestinal (GI) tract receptors human intestinal peptide-associated transporter (HPT1), hPEPT1, D2H and human sucrose-isomaltase complex (hSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the bloom in vivo delivery, particularly for treatment or prevention
                                                                                                                                                                                                                                                                            of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, migraine, or angina pectoris. Specifically they are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (I) may also provide targeting to the GI tract. Other uses of (I) are: (1) to determine the level of specified receptors in a sample (in a binding assay); and (11) to screen for molecules that bind (I): "Immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and measure (I), e.g. for imaging, monitoring treatment, tissue analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chantibodies, used to deliver therapeutic or diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HPT-1 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cherapeutic agent delivery; therapy; probe.
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                                                                                                 EIHVKVKDINDNPP
                                                                                                                    ECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                 also for peptide purification and nce 832 AA;
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10; Conserv
               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                787
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                                                                                                                                                                  Conservative
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                  Protein; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                 338
                                                                                                                                  15
                                                                                                                                                                                59.1%;
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cagney GM, Carter JM, Lambkin A, Singleton J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60;
Pred. No.
                                                                                                                                                                                Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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0.049;
                                                                                                                                                                                                                                                                  immobilisation.
                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                               Length 832
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    chimaeras and
ostic agents to,
or leuprolide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blood)
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RESULT
RE

WO9600289-A1. Rattus rattus.

catenin; therapy; clone.

Protocadherin; pc3; pc4; pc5; human; Protocadherin clone RAT-224

rat;

cadherin; cell adhesion;

R87107;

R87107 standard; Peptide;

43

3

28-AUG-1996

(first entry)

04-JAN-1996. 26-JUN-1995; 27-JUN-1994;

26-JUN-1995; U08071. 27-JUN-1994; US-268161. (DOHE-) DOHENY BYE INST

Suzuki WPI; 96

96-068873/07 DB; T03582.

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29

CKIIKVVDVNDNAP

1 CECNIKVKDVNDNFP 15

Similarity

Conservative

0

Gaps

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CC C-terminus of the fourth extracellular subdomain (EC-4) were CC designed for use as PCR primers. PCR was carried out on a rat brain CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CC The 450 bp band corresponded to the expected length between the two CC primer sites, but the 130 bp band could not be predicted from any CC primer sites, but the 130 bp band could not be predicted from any CC clones were extracted and sequenced. Nineteen novel partial cDNA CC clones (including sequences corresp. to the PCR primers) are given CC clones (including sequences corresp. to the PCR primers) are given CC clones were isolated. The DNA and deduced AA sequences of the CC clones were isolated at S8860-R58878. The deduced AA sequences of the CC clones were isolated to the pCR primers) are given CC clones (including sequences corresp. to the PCR primers) are given CC cadherins. The cadherins described thus far have highly conserved CC D-Y-E or D-E-F located at the middle region of the subdomain and CC the consensus sequence in R58879 or R58800 at its end, while the CC corresp. sequences of other subdomains, except for the 5th extra-CC cellular subdomain (EC-5), are D-R-E and the sequence in R58881 cc clones that corresp. to cadherin extracellular subdomains include the sequence D-Y-E or D-F-E at one end, but have the sequence CC D-Y-N-D-N-X-P-X-F instead of R58879 or R58880 at the other end. CC chass appear to comprise a new subclass of cadherin-related collars to comprise a new subclass of cadherin-related
Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q68957.

Polynuclectide sequences encoding new proto:cadherins - useful for modulating natural binding and regulating activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for modulating natural binding and regulating activities.

Example; Page 38; 114pp; English.

Two regions of conserved AA sequence, one from the middle of the third cadherin extracellular subdomain (EC-3) and the other from third cadherin extracellular subdomain (EC-3) and the other from third cadherin extracellular subdomain (EC-3) and the other from third cadhering the subdomain (EC-3) and the other from third cadhering the subdomain (EC-3) and the other from third cadhering the subdomain (EC-3) and the other from the subdomain (EC-3) and the subdomain (EC-3) are subdomain (EC-3) and the subdomain (EC-3) and the subdomain (EC-3) are subdomain (EC-3) and the subdomain (EC-3) are subdomain 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1995
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US-998003.
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                                                                                                                                                                                       A
                                   56.8%;
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   Score 50; DB
Pred. No. 0.08
1; Mismatches
                                       DB 1;
0.085;
                                                                          Length 43;
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PT New isolated vascular endothelial cadherin-2 - used to develop products for modulating angiogenesis, e.g. for treating tumours, proglaucoma, psoriasis, inflammatory diseases or organ transplantation program is provided by the sequence is that of protocadherin-4 (pcdh-4), or as it may call the sequence is that of protocadherin-2. As a vascular endothelial cadherin it promotes cell-to-cell homotypic adhesion and its cadherin it promotes cell-to-cell homotypic adhesion and its capression is upregulated in proliferating endothelial cells in comparison to resting cells. It can be used for inhibiting cappeners and inhibiting pathological conditions such as tumours, angiogenesis and inhibiting pathological conditions such as tumours, can discovered in the pathological conditions such as tumours, and soriasis. It may also be used for the prevention or inhibition of cell eukocyte infiltration, tumour cell metastasis, or endothelial permeability, as a vaccine and for making endothelial junctions more permeable to antigens, thus indicating use of the modifiers for treatment or prevention of acute and chronic inflammatory diseases, or organ transplantation, myocardial ischaemia, atherosclerosis, rheumatoid carthritis and intestinal infection. It may also be used for detection, sequence 1180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 40; 146pp; English.

CC 887102-887120 represent partial fragments of the rat protocadherin CC sequence. The CDNAs encoding these sequences were isolated after CC screening a rat brain cDNA preparation with the primers shown in T03575 CC and T03576. The primers were constructed from portions of the amino acid CC sequences of the third and fourth extracellular domains of published CC catherin sequences. The full length cDNA sequence encoding rat CC catherin sequences with the cytoskeleton through catenins and other CC catherin interacts with the cytoskeleton through catenins and other CC catherins adherins, but in those which possess it, it is essential for the CC catherins adhesive function. The catherins which do not possess a CC cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in CC cell-cell as the cell-cell adhesive properties. Antibodies produced CC call, as well as the cell-cell adhesive properties. Antibodies produced CC these protocatherins, and can be used therapeutically.
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Best Local Similarity
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podh-4 gene; VE-cadherin; protocadherin-4; VE-cadherin-2;

podh-4 gene; VE-cadherin; protocadherin-4; VE-cadherin-2;

vascular endothelial; angliogenesis; modulation; glaucoma; psoriasis;

inflammatory disease; organ transplantation; treatment; inhibition;

tumour; metastasis; rheumatoid arthritis; diagnosis; detection;

cell adhesion; atherosclerosis; myocardial ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-348441/30.
N-PSDB; V27593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1997; U20006.
12-DEC-1996; SE-004731.
(IMCL-) IMCLONE SYSTEMS
Dejana E, Telo P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide(s) encoding human protocadherins pc3
pc5 - involved in cell-cell adhesion and regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-1998 (first entry)
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Pred. No. 0.085;
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RESULT R87117

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CTVSIQVVDVNDNAP CECNIKVKDVNDNFP

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Mismatches

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                                                                                                                             DR N-PSDB; 068967.

Dr Polynuclotide sequences encoding new proto:cadherins - useful proto: modulating natural binding and regulating activities. PS Example; Page 44; 114pp; English.

CC Two regions of conserved AA sequence, one from the middle of the CC third cadherin extracellular subdomain (EC-3) and the other from the CC third cadherin extracellular subdomain (EC-4) were CC designed for use as PCR primers. PCR was carried out on a rat brain CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. Two major bands of about 450 bps and 130 bps were found. CDNA prepn. The collect and sequences. The 450 bp and 130 CD bp bands were extracted and sequenced. Nineteen novel partial cDNA CC clones (including sequences corresp. to the PCR primers) are given CC clones (including sequences corresp. to the PCR primers) are given CC consensus sequence in R58870. The deduced AA sequences of the corresp. Sequences in the EC-3 including the consensus sequence CC corresp. Sequences of cher subdomains, except for the Sth extracellular subdomain subdomain and the CC-3) are D-R-E and the sequence in R5881 CC sequence D-Y-E or D-F-E at one end, but have the sequence CC the sequence D-Y-E or D-F-E at one end, but have the sequence CC the sequence D-Y-E or D-F-E at one end, but have the sequence CC DNAs appear to comprise a new subclass of cadherin-related CC DNAs appear to comprise a new subclass of cadherin-related CC DNAs appear to comprise a new subclass of cadherin-related CC DNAs and the consensus sequence and consensus sequence
Query Match
Best Local S
Matches 9
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DOHE-) DOHENY EYE
Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-1994.
23-DEC-1993; U12588.
29-DEC-1992; US-998003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cadherin; cell adhesion molecule.
Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R5887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R58875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat-352 cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 CKYLIKYLDYNDNAP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CECNIKVKDVNDNEP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94-293849/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 41
Similarity 60.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partial sequence.
                     54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą
                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                     ; DB 1;
. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
3.3;
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                                        Length 41
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pr polynuclectide(s) encoding human protocadherins pc3 and pc4 and rat pr pc5 - involved in cell-cell adhesion and regulation activities
PS Example 1; Page 47; 146pp; English.

CC R87102-R87120 represent partial fragments of the rat protocadherin
CC sequence. The cDNAs encoding these sequences were isolated after
CC screening a rat brain cDNA preparation with the primers shown in T03575
CC screening a rat brain cDNA preparation with the primers shown in T03575
CC cand T03576. The primers were constructed from portions of the amino acid
CC cadherin sequences. The full length cDNA sequence encoding rat
CC coadherin sequences. The full length cDNA sequence encoding rat
CC coadherin interacts with the cytoskeleton through catenins and other
CC cytoskeleton associated proteins. The cytoplasmic domain of
CC cytoplasmic domain appear to function via a different method from those
CC with a cytoplasmic domain appear to function via a different method from those
CC with a cytoplasmic domain. These protein sequences are involved in
CC cell, as well as the cell-cell adhesive properties. Antibodies produced
CC against these sequences are useful for modulating the binding activity of
CC these protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 9
                                                                                                                                      17-APR-1992; 872643.
17-APR-1992; US-872643.
19-APR-1993; US-040460.
26-JAN-1994; US-188228.
(DOHE-) DOHENY EYE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DOHE-) DOHENY EYE INST. Suzuki S;
WPI; 96-068873 /^~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R87117 stand
R87117;
28-AUG-1996
                                                                                                                                                                                                                                                            Full length human cadherin-5.
Full length human cadherin-5.
Ca2+ dependent; cell adhesion protein; placental; cac
Ca2+ dependent; cell adhesion; determination;
brain; human; antibody; purification; determination;
brain; human; antibody; purification; calcium ion.
 Claim 5; Columns 75-78; 59pp; English.
The present sequence is full length human cadherin-5, which is a Ca2+ dependent cell adhesion protein. The human cadherin was isolated from a placental cDNA library, using probes based
                                                                                                                                                                                                                                                                                                                             W13130 standard; Protein; W13130; 13-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T03592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-1995; U08071.
27-JUN-1994; US-268161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catenin; therapy; clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protocadherin; pc3;
                                                                             Antibodies
                                                                                              N-PSDB; T61921.
                                                                                                                         Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protocadherin clone
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                    8-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTVSIQVVDVNDNAP
                                                                                                           97-108328/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 60. 9; Conservative
                                                                             င်
                                                                            cadherin
                                                                                                                                                                                                                                                                                                               st entry)
cadherin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pc4; pc5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                            proteins -
                                                                                                                                                                                                                                                                                                                                                              780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1;
Pred. No. 0.17;
2; Mismatches
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                                                                             useful as
                                                                             cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 41
                                                                                                                                                                                                                                                                                                  cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                             antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                   CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT W13126 ID W1 AC W1

14

W13126; W13126;

standard;

Protein;

799

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135 IKVHDVNDNWP 145

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35558<u>8</u>
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                                                                                                      50
                                                                                                                            Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
claim 1; Column 69-72; 56pp; English.
This sequence represents human cadherin-5. The invention specifically
provides details of human cadherin-5, -8, -11, -12 and -13, and rat
cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell
adhesion proteins. They are glycosylated integral membrane proteins
that have an N-terminal extracellular domain that determines binding
specificity, a hydrophobic membrane spanning region and a C-terminal
cytoplasmic domain, which is highly conserved among members of the
superfamily. The C-terminal domain interacts with the cytoskeleton
through eatenins and other cytoskeleton-associated proteins. The
novel cadherin proteins may be used in the analysis of the role of
cadherins in various cancers. Sequence analysis of the cadherin
cadherin. The cadherin proteins may be isolated by using anti-cadherin
cadherin and to determine the tissue specific distribution of cadherin
proteins. Each subclass of cadherins has a unique tissue distribution
                              Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-1997.
17-APR-1992; 872643.
19-APR-1993; US-049460.
17-APR-1992; US-872643.
01-NOV-1994; US-332638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on homologous rat cadherin cDNA.
Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-362997/33.
N-PSDB; T85401.
                                                                                                     Sequence
                                                                                                                   pattern
                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     superfamily; cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cadherin; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cadherin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W25634
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOHE - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 IKVHDVNDNWP 145
   5 IKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 IKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conserv
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOHENY EYE
                                                                                                      780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded by AAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                           54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calcium-dependent cell adhesion protein; eatenin; cancer.
                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
Pred. No.
                                           Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4;
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                                                            밁
                                                         μ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                         Length 780;
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                               Gaps
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Best Local Similarity 72.7
Matches 8; Conservative
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28-JAN-1997.
17-APR-1992; 872643.
17-APR-1993; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
Example 2; Columns 85-90; S9pp; English.

The present sequence is full length human cadherin-8, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA us isolated from a foetal brain cDNA library, using probes based on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 793 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Columns 49-52; 59pp; English.

The present sequence is full length rat cadherin-8, which is a Ca2+ dependent cell adhesion protein. The rat cadherin cDNA was isolated from a brain cDNA library using a labelled rat cadherin-8 extracellular domain PCR fragment as a probe. The rat cDNA was then used to isolate the cDNA encoding its full length human homologue from a human foetal brain cDNA library.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 799 AA;
                                                                                                                                                                                             Suzuki
WPI; 97
                                                                                                                                               etc.
                                                                                                                                                      N-PSDB; T61923.
Antibodies to cadherin proteins - useful as cadherin antagonists,
                                                                                                                                                                                                                                                                                                                                             14-MAY-1997 (first entry)
Full length human cadherin 8.
Ca2+ dependent; cell adhesion protein; foetal; cadherin; rat; brain; human; antibody; purification; determination; tissue expression; binding antagonist; calcium ion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1997 (first entry)
Full length rat cadherin-8.
Ca2+ dependent; cell adhesion protein; foetal; cadhe brain; human; antibody; purification; determination; tissue expression; binding antagonist; calcium ion.
                                                                                                                                                                                                                                    17-APR-1992; 872643.
17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
US5597725-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                W13132 standard; Protein; 793 W13132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-108328/10.
N-PSDB; T61917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus rattus.
                                                                                                                                                                                                                         (DOHE-) DOHENY EYE INST.
                                                                                                                                                                                                                                                                                                     28-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 IKVQDINDNAP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DOHE-) DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                        k1 S;
97-108328/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKVKDVNDNFP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins - useful as cadherin antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foetal; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                         Query Match
Best Local Similarity
                                  Matches
5 IKVKDVNDNFP 15
|||:|:||| |
148 IKVQDINDNAP 158
                                   8
                                   Conservative
                                           52.3%;
72.7%;
                                   ..
                                           Score 46; I
Pred. No. 9.
                                   Mismatches
                                           9.6;
                                                   1;
                                                   Length 793;
                                  Indels
                                  0;
                                  Gaps
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Search completed: January Job time: 1684 sec ģ 2000, 15:40:37 밁

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Number of hits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-991-628-6
82
1 SARTLNNRYTGPYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    January
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188963 seqs, 23686106 residues
       100
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Mouse CRF RB1 rece
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Matches 15
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US7798918-A.

15-DEC-1992.

27-NOV-1991; 798918.

27-NOV-1991; US-798918.

(USSH) US DEPT HEALTH & H

Amagai M, Klaus-Kovtun V,

WPI; 93-057435/08.
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R30742;
   rused protein recognised by pemphigus vulgaris auto:antibody useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.

NOT908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human 1gGl hinge region and the resulting fusion protein is useful to treat or diagnose
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N-PSDB; Q35992.

DNA encoding pemphigus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.

This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.

Sequence 999 AA;
                                                                                                                                                                          30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                    Pemphigus vulgaris antigen protein extracellular region Autoantibody; immunoglobulin G; IgGl; fusion protein; ditreatment; pemphigus vulgaris; PV; bulla; blister; skin
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Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein; cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                       W07908;
29-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                 Homo sapiens.
J08188540-A.
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Pred. No. 2.1e-06;
Mismatches 0;
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in disease;
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Best Local :
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Best Local
signal transduction.
Mus sp.
Key Loca
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Sequence
                                          Mouse CRF RB1 receptor. Corticotropin releasing factor receptor; CRF-R; corticoliberin;
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Strominger JL, Wucherpfennig KW;
WPI; 96-425218/42.
                                                                                               R97293 standard; Protein; 431
R97293;
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W09627387-A1.
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human papillomavirus; Epstein-Barr virus; DNA polymerase;
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                                                                           21-AUG-1996 (first entry)
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07-MAR-1995; US-400796
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614 AA;
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    implicated in autoimmune disease
antigen; autoimmune disease;

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1.2e-06;
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13-JUN-1996.
06-DEC-1995; US-353537.
17-JAN-1995; US-374009.
(SALK ) SALK INST BIOLOGICAL STUDIES.
(SALK ) SALK INST BIOLOGICAL STUDIES.
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                                                                                                          08-APR-1996 (first entry)
Rat CRF2-beta receptor.
CRF2-beta receptor; corticotropin-releasing
cerebrovascular disorder; memory disorder; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse corricotropin releasing factor receptor mCRF-RB1 was identified as the product of a cDNA clone (T28972) isolated fromouse heart library. Recombinant mCRF-RB1 can be expressed in host cells transformed by the cDNA clone. The receptor can be to identify agonists and antagonists that modulate the signal transduction activity mediated by CRF receptors. It may be administered therapeutically to reduce high ACTH levels caused
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118. .138
/label= Transmembrane_domain
139. .147
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105
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Pred. No.
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14-JUN-1994;
14-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                   Corticotropin-releasing factor-2 receptor, and DNA encoding it used to isolate CRF-2 receptor antagonists for the treatment of cerebrovascular disorders, memory disorders and Alzheimer's displications. Page 63-66; 109pp; English.

Rat corticotropin releasing factor-2-beta (CRF2-beta) receptor (R90575) is a membrane-bound G-coupled protein receptor involve in signal transduction. It can be produced by expression of
                                                                                                                                                                                               encoding cDNA (T12244) in procaryotic or eucaryotic host cells. Recombinant CRF2 receptor is used to screen CRF2 receptor agonists and antagonists of therapeutic appln., and to prepare antibodies which specifically bind to CRF2 receptors.

Sequence 431 AA;
11-AUG-1995;
18-AUG-1994;
21-NOV-1994;
                                Kaposi's sarcoma
WO9606159-A1.
                                              therapy
                                                    Kaposi's sarcoma;
                                                                            R93616 standard; Protein; 454 R93616;
                                                                                                                                                                                                                                                                                             N-PSDB; T12244.
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Lovenberg TW, Oltersdorf T;
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                                                                                                                           RTTTRNFSGPYSY
                                                                                                                                                          Similarity 38.5; Conservative
                                                                                                                                                                                                                                                                                                                                  US-259959.
US-381433.
US-485984.
US-292365.
US-343100.
                                                                     (first entry)
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                                                     Lymphoma;
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                                      herpesvirus
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                                                     ORF32 product. vaccine; diagn
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Query Match
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Sclaim 17: Page 235-237: 305pp; English.

Kaposi's sarcoma associated herpes virus (KSHV) clone KS5 (T16806)

Cobtd. from a KS lesion genomic library, includes 15 complete ORFs 2 incomplete ORFs (T16807-23) named according to their herpesvirus caimiri positional homologues. The ORF32 (T16802) product is given in R93616. KSHV proteins and peptides may be obtd. by incorporating encoding sequences into a vector and expression in concorporating encoding sequences into a vector and expression in construct or therapeutic value.

Sequence 454 AA;
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(UYCO) UNIV COLUMBIF
(GRAN/) GRANT D E.
(VIEL/) VIELE L.
Chang Y, MOOTE PS,
                                                                                            raising a
                                                                                                        respectively) of the bacterial host cells raising antibodies.
                                                                                                                                                                 N-PSDB; T30694.

Herpes virus associated with Kaposi's sarcoma - also definitive DNA sequences, useful for diagnosis of and to develop prods. for treatment of Kaposi's sarcoma Claim 17; Page 188-189; 277pp; English.

Claim 17; Page 188-189; 277pp; English.

Lambda clone KS5 (T3069) is a fragment of a newly identified human gamma-2 herpesvirus associated with Kaposi's sarcoma (KS). KS5 has 17 open reading frames (T30682-98), 15 of which are complete, including ORF32 (T30694). The protein products (R97830-46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaposi's sarcoma associated herpesvirus ORF32
Kaposi's sarcoma; gamma-2 herpesvirus; KSHV; t
vaccine; diagnosis; AIDS.
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V-1994; US-343101.
R-1995; US-420235.
) UNIV COLUMBIA NE
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Similarity 54.5%;
6; Conservative
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 6,
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 Score 37; DB Pred. No. 77; 1; Mismatches
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PP 1:
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Matches 8
                              17-SEP-1990; 062569.

18-SEP-1989; US-408339.

01-MAR-1990; US-487181.

(SYNE-) SYNERGEN INC.

WPI; 91-133285/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA encoding enzyme for fragmenting N-acetyl:heparosan giving products useful as pharmaceutical starting material, also related protein, vector, transformed cells, etc.

Claim 2; Page 38-40; 54pp; French.
An enzyme which degrades high mol. wt. N-acetylheparosan into fragments of lower mol. wt. We consider the same pharmaceutical starting materials) can be obtained from E.coli (K5) SEBR 3282. The DNA sequence (Q86268) coding for the enzyme was isolated in a plasmid (p838.7) which has been deposited in E.coli RRI strain as CNCM I-1352. The deduced amino acid sequence (R71802) has homology with an exo-poly-alpha-D-galacturonidasse from Erwinia chrysanthemi sequence 820 AA;
                                                                                                                                                                                                                                                                                R12098;
                                                                                                                                                                                                            22-JUL-1991 (first entry)
Haem 84-1 portion of H.conto
Parasitic nematode; vaccine;
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24-FEB-1995.
17-AUG-1993; 010050.
17-AUG-1993; FR-010050.
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Legoux R, Lelong P, Salome
WPI; 95-100554/14.
N-PSDB; Q86268.
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                                                                                                                                                                                                                                                                                                     standard;
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li (K5) SEBR 3282 (CNCM I-1013)
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/note= "Asn-X1-X2-Ser motif (X1=Ile, Leu or T
and X2-Val, Ile or Ala)"
495. 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Asn-X1-X2-Ser motif (X1=Ile,
and X2=Val, Ile or Ala)"
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and X2=Val, Ile or Ala)"
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and X2-Val, Ile or Ala)"
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and X2=Val, Ile or Ala)"
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                                                                                                                                                                                                               H.contortus 
vaccine; Hc.
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1; Mismatches
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hes 1;
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                DRAPED OKKETO
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Best Local S
Matches 6
QUIN-1990; NL0092.
QUIER-) CENT DIEMGENEESKUND.
MOOIMAN R, Wensvoort G;
WPI; 91-036746/05.
P-PSDB; Q1035
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Best Local
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18-SEP-1989; US-408339.

01-MAR-1990; US-487181.

(SYNE-) SYNERGEN INC.

WPI; 91-133285/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; 011799.

Protein from Haemonchus contortus and other nematodes -
therapeutic and prophylactic agent to protect plants, an
therapeutic and prophylactic agent to protect plants, an
humans from parasitic nematode infection.

Disclosure; Fig 49; 209pp; English.

The proteins derived from the nematode DNA may be used t
vaccines against parasitic infection of plants, humans a
esp. sheep. MAbs may also be raised to provide passive t
prophylaxis against infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein from Haemonchus contortus and other nematodes - therapeutic and prophylactic agent to protect plants, a humans from parasitic nematode infection.

Disclosure; Fig 49; 209p; English.

The proteins derived from the nematode DNA may be used vaccines against parasitic infection of plants, humans esp. sheep. MAbs may also be raised to provide passive prophylaxis against infection.
                                                                                                                                                                                                          Hog cholera virus genome product.
Swine fever virus; HCV; pestvirus; border disease
Bovine viral diarrhoea virus; BVDV; Togaviridae; s
                                                                                                                                                                                                                                                                                                     R10473 standard;
R10473;
                                                                                                                                                                                            Hog Cholera Virus.
                                                                                                                                                                                                                                                                                09-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haem 84-2 portion of H.conto
Parasitic nematode; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R12099;
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6; Conserv
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                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                            Protein;
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Vaccine; Hc.
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Pred. No. 1.3e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1;
Pred. No. 1.2e+02;
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Length 480

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W31545
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Best Local Similarity
""" Conserv
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                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                 propersing Bloom's syndrome, and carriers, by detecting mutant BLM genes - for gene therapy with nucleic acid encoding active BLM protein to treat Bloom's syndrome and cancer in general protein to treat Bloom's syndrome and cancer in general protein to treat Bloom's syndrome and cancer in general protein to treat Bloom's syndrome and cancer in general protein is used in diagnosing Bloom's syndrome where 2 mutated BLM genes CC This is used in diagnosing Bloom's syndrome where 2 mutated BLM genes CC This is used in diagnosing Bloom's syndrome where 2 mutated BLM genes CC is detected. The BLM gene is in the 250 kb region between two markers CC is detected. The BLM gene is in the 250 kb region between two markers CC isolated. The BLM gene is in the 250 kb region between two markers (1901ated). The longest clone H1 was isolated and used to screen a Hela cDNA CC ilbrary. The longest clone H1 was isolated and extended by PCR to isolate this BLM gene sequence. Delivery of a functional BLM gene to bone marrow CC this Blom's syndrome. Identification of the BLM gene and its products should assist in the development of therapeutic and diagnostic agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY:199; U19046.
15-NOV-1995; US-559303.
(NYBL-) NEW YORK BLOOD CENT
Ellis N, German J, Groden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The genome sequence and its encoded product are sufficiently similar to other pestviruses of the family Togaviridae, that they may be used in vaccination and diagnosis of pestvirus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W15264 standard; Protein; 1418 W15264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T67013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; diagnosis; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLM; Bloom syndrome; BS; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloom syndrome active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Fig 1; 33pp; English.
                             Bloom's syndrome BLM mutated protein.
BLM; Bloom's syndrome; BS; mutant; tr
                                                                              W31545
                                                                                          W31545 standard;
                                                                                                                                                                                                                                                                                                         Sequence
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                  Homo sapiens
                                                             27-JAN-1998 (first entry)
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SARTLNNK 24
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7; Conserv
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                                                                                                                                                                                                                                                                                                           1418 AA;
                                                                                                                                                                                                                                Conservative
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                                                                                            Protein; 185 AA
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                                                                                                                                                                                                                                               43.9%;
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                               mutant; truncation; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred. No.
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                                                                                                                                                                                                                                              Score 36; DB 1;
Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                 Mismatches
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1.3e+03;
3;
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                                                                                                                                                                                                                                                              Length 1418;
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CC This is a truncated BLM protein encoded by a mutant gene sequence isolated from a Japanese Bloom's Syndrome sufferer designated "97(AsoK)". The deletion of CAA from positions 631-633 of the CC wild-type gene results in a stop codon at amino acid position 186. This was one of the seven unique mutantions which were identified in a study of 10 people with Bloom's Syndrome. Based on the various mutations, diagnostic tests for Bloom's Syndrome have been developed which use standard sequence analysis techniques to detect the presence of 2 mutated BLM genes or the absence of a wild-type BLM gene.

CC Note: The present sequence does not appear in the specification; it has been made by modifying the H1-5' wild type BLM sequence which is provided in Figure 2 (W15264).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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22-MAY-1997, U19046.
15-NOV-1996; U5-559303.
(NYBL-) NEW YORK BLOOD CENT IN Ellis N. German J. Groden J. WPI: 97-289051/26.
Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM genes - for gene therapy with nucleic acid encoding active BLM genes - for gene therapy with nucleic acid encoding active BLM protein to treat Bloom's syndrome and cancer in general Disclosure; Page -; 51pp; English.

This is a truncated BLM protein encoded by a mutant gene sequence isolated from a German Bloom's Syndrome sufferer designated "112(NaSch) The substitution of the base A at the position 888 of the wild type H1. gene to the base T results in a stop codon at amno acid position 272. This was one of the seven unique mutations which were identified in a study of 10 people with Bloom's Syndrome. Based on the various
                                                                                                                                                                                                                                                                                                                                                                                                            Bloom's syndrome BLM mutated protein.
BLM; Bloom's syndrome; BS; mutant; tr
                                                                                                                                                                                                                                                                                                                                                                                                                                             W31546 standard; Protein; W31546; 27-JAN-1998 (first entry)
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N-PSDB; T93389
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                                                                                                                                                                       N-PSDB; T93390
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15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-559303.
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/note-
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OD CENT
                                                                                                                                                                                                                                                                                                 "Truncated protein. The substitution of the base at the position 888 of the wild type H1-5' gene to the base T results in a stop codon at amino acid position 272"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Truncated protein. The nucleotide positions (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               truncation; therapy; diagnosis
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31-633 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of CAA
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                                                                      112 (NaSch) "
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Best Local Similarity 87.9
Matches 7; Conservative
                                                                         Matches
                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-1995; US-559303.
(NYBL-) NEW YORK BLOOD CENT INC.
Ellis N. German J. Groden J;
WPI; 97-289051/26.
N-PSDB; T93391.
                                                                                                                                                               This is a truncated BLM protein encoded by a mutant gene sequence isolated from a Japanese Bloom's Syndrome sufferer designated "93(YoYa)". The insertion of a bp A at the position 1610 in the wild type H1-5' BLM gene results in the insertion of a novel codon for Lysine after amino acid position 514 followed by a stop codon.

This was one of the seven unique mutations which were identified in a study of 10 people with Bloom's Syndrome. Based on the various mutations, diagnostic tests for Bloom's Syndrome have been developed which use standard sequence analysis techniques to detect the presence of 2 mutated BLM genes or the absence of a wild-type BLM gene of Note: The present sequence does not appear in the specification; it has been made by modifying the H1-5' wild type BLM sequence which is provided in Figure 2 (W15264).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutations, diagnostic tests for Bloom's Syndrome have been developed which use standard sequence analysis techniques to detect the presence of 2 mutated BLM genes or the absence of a wild-type BLM gene. Note: The present sequence does not appear in the specification; it has been made by modifying the HI-5' wild type BLM sequence which is provided in Figure 2 (WI5264).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM genes - for gene therapy with nucleic acid encoding active BLM protein to treat Bloom's syndrome and cancer in general Disclosure; Page -; Sipp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bloom's syndrome BLM mutated protein.
BLM; Bloom's syndrome; BS; mutant; truncation; therapy; diagnosis.
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||||||:
17 SARTLNNK 24
                                                                         Local Similarity 87.1 hes 7; Conservative
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                 SARTLNNR 8
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1. .515
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the wild type H1-5' BLM gene results in the
insertion of a novel codon for Lys after amino
acid position 514 followed by a stop codon"
                                                                                           43.9%;
87.5%;
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Pred. No.
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1 SARTLNNRYTGPYT
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A;Accession: A41088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: pemphigus vulgaris antigen (; Species: Homo sapiens (man) (; Species: Homo sapiens (man) (; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 (; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 (; Accession: A41088 R; Amagai, M.; Klaus-Kovtun, V.; Stanley, J.R. (cell 67, 869-877, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-999 < AMA>
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Matches 15
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Result

Database Searched: Title:

Run on

extensin homolog F hypothetical prote

## ALIGNMENTS

#text\_change 22-Jun-1999

PID:g190752

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F;50-99/Product: desmoglein homolog #status predicted F;50-615/Domain: extracellular #status predicted <EXTS F;52-157/Domain: cadherin repeat homology <CR1> F;160-267/Domain: cadherin repeat homology <CR3> F;270-383/Domain: cadherin repeat homology <CR3> F;270-383/Domain: cadherin repeat homology <CR3> F;390-495/Domain: cadherin repeat homology <CR4> F;496-598/Domain: cadherin repeat homology <CR5> F;616-639/Domain: transmembrane #status predicted <TMM> F;640-999/Domain: intracellular #status predicted <TMM> F;640-999/Domain: in
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: C70333
                                                                                                                                                                                                                     RESULT 2
C7033
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C7Species: Aguifex aeolicus
C7Species: Aguifex aeolicus
C7Species: Aguifex aeolicus
C7Date: 08 May-1998
C7Accession: C70333
C7Accession: C70333
C7Accession: C70357
R7Deckert, G.; Warren, P.V.; Gaasterland, T.; Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;910-938/Domain: desm
F;937-966/Domain: desm
F;110,180,545/Binding
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desmoglein repeat <DG2>
ding site: carbohydrate
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0; Mismatches
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2e-06;
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A;Experimental source: strain H37Rv
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A;Residues: 1-531 AADF>
A;Cross-references: GB:AE000686; NID:g2983038; PID:g2983043; GB:AE000657
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               retrovirus-related pol polyprotein pseudogene -
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 04-Jan-1
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A:Accession: B70854
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A; Residues: 1-163 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Rv2991 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rajandream, M.A.; Rogers, Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                     Hirose, Y.; Takamatsu, irology 192, 52-61, 1993, Title: Presence of environments
                                                                                                                                                                                                                                                     Reference number: A44282; MUID:93297138 in members of the Accession: A44282
                                                                                                         ;Keywords: pseudogene
;45/Region: opal stop codon
;485/Region: opal stop codo
                                                                                                                                                                                :Cross-references: GB:D10083
                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-848 <HIR>
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Pred. No.
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Pred. No. 2.2;
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C28A5.4 protein (clone C28A5) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 17-Oct-1997
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A;Status: preliminary
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nosories: 1-2262 <KAW>
A;Cross-references: EMBL:X57559; NID:g61985; PIDN:CAA40788.1; PID:g61991
A;Cross-references: EMBL:X57559; NID:g61985; PIDN:CAA40788.1; PID:g61991
C;Superfamily: parainfluenza virus RNA-directed RNA polymerase
8
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S16664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Okazaki, K.; Tanabayashi, K.; Takeuchi, K.; Hishiyama, M.; Okazaki, K.; Yamada, A. Virology 188, 926-930, 1992
A;Title: Molecular cloning and sequence analysis of the mumps virus gene encoding the A;Reference number: A42548; MUID:92263804
A;Accession: A42548
                                                                                                                                                                                                                                                                               R;Kawano, M.; Okamoto, K.; Bando, H.; Kondo, K.; Tsurudome, Nucleic Acids Res. 19, 2739-2746, 1931. A;Title: Characterizations of the human parainfluenza type A;Reference number: S16659; MUID:91252221
                                                                                                                                                                                                                                                                                                                                                         large protein L - parainfluenza virus type 2
C;Species: parainfluenza virus type 2
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Jun-1999
C;Accession: S16664
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A;Residues: 1-2261 <OKA>
A;Cross-references: GB:D10575; NID:g222145;
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N;Alternate names: L protein
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Best Local S
Matches 8
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ARTLNRMYGVPHLF
                                 ARTLNNRYTGPYTF 15
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                                                                   Similarity 57.8; Conservative
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                                                                     Score 39; DB 2;
Pred. No. 1.9e+02;
1; Mismatches 5
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Pred. No.
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1.9e+02;
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C; Accession: S435//
R; Palmer, S.
submitted to the EMBL Data
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                                                                                                                                          C:Species: Saccharomyces cerevisiae
C:Date: 28-May-1993 *sequence_revision 28-May-1993 *text_change
C:Accession: S25196; S49960; S35357
R:Maarse, A.C.; Blom, J.; Grivell, L.A.; Meijer, M.
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                                                                                                                                                                                                                  mitochondrial import protein MPII precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YI3299.09; protein YIL022w
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                                                                                A; Reference number: A; Accession: S25196
                                                                                                                   A; Title: MPI1,
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A; Introns: 257/1;
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                                              A; Molecule type: DNA
A; Residues: 1-431 < MAA>
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A;Experimental source: cultivar Columbia
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A; Accession: T01862
              A;Cross-references: EMBL:X67276; NID:g3966; PID:g3967
R;Skelton, J.; Churcher, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Experimental source:
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\;Residues: 1-973 <H
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Langston, Y.; Stoneking, T.; Drone, K.; Ames, he EMBL Data Library, July 1998
The sequence of Arabidopsis thaliana T7M24.
                                                                                                                   an essential
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53.8%;
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2; Mismatches
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December
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73;
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18;
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A;Map position: 9L
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A;Residues: 82-89;112-122;221-228;295-306;316-327;356-370 <HOR>
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A;Residues: 1-43
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                                                     Query Match
Best Local Similarity
7; Conserv
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/Reywords: ATP
/39-313/Domain: protein kinase homology <KIN>
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Best Local Similarity
Matches 8; Conserv
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Horst, M.; Jenoe, P.; Kronidou, N.G.; Bolliger, L.; Oppliger, W.; Sch
                                                                                                                                                                                                                                                                                           ;Molecule type: DNA
;Residues: 1-865 <H
                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Saccharomyces cerevisiae
| Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 24-Sep-1999
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575 SSQTLNQRDTSPF
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3035-3041, 1993
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nilarity 53.88;
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                                                                 Score 38; DB Pred. No. 96; 3; Mismatches
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sauvagine/corticotropin-releasing factor receptor C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #C:Accession: I49279

#text\_change

26-Aug-1999

mouse

R; Kishimoto, T.; Pearse, R.V. Proc. Natl. Acad. Sod. U.S.A. 92, 1108-1112,

A; Title: A sauvagine/corticotrop

149279;

MUID:95166778

1995 factor

receptor

expressed in

heart and.

A; Reference

RESULT 149279

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable glucose-1-phosphate thymidylyltransferase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 29-Sep-1999
C;Accession: F71151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-431 <KIS>
A;Cross-references: EMBL:U21729; NID:g717137; PID:g717138
C;Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv0043c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998 C;Accession: C70912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP000002; NID:g3236129; A;Experimental source: strain OT3 A;Note: this accession replaces an interim acce C;Genetics:
A;Gene: PH0413
C;Superfamily: mannose-1-phosphate guanylyltrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of
A;Reference number: A71000; MUID:98344137
A;Accession: F71151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida,
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A; Residues: 1-244 <COL>
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A; Residues: 1-356 < KAW>
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Best Local :
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les 6; Conserv
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        Similarity
                                                                                                                          nces: GB:Z80775; GB:AL123456; source: strain H37Rv
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                                                                                                                                             PID:e268216; PID:g1568582
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C;Accession: E69312

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Accession: E69312

A;Accession: E69312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gr.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holl Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987

A;Accession: B70931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitrate reductase gamma subunit homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-423 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: I -332 < KLE> A;Cross-references: GB:AE001069; GB:AE000782; NID:g2689392; PID:g265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AL022021; GB:AL123456; A;Experimental source: strain H37Rv
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Result
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   SARTLNNRYTGPYTF
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Copyright (c) 1993 - 1998 Compugen
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RRPL_P12HT
CRF2_MOUSE
SYLC_SCHPO
Y0H6_MYCTU
YDJ1_SCHPO
   ASPP_AEDAE
ESC1_SCHPO
SYRM_YEAST1
YDAK_ECOLI
BLM_HUMAN
C6B2_HELIAM
C6B2_HELIAM
C6B2_HELIAM
C6B1_POVMK
COND_NEUCR
POL4_DROME
POL4_DROME
RRPL_SV41
YG08_BPT4
VG08_BPT4
V
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GA6B_XENLA
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(without alignments)
15.282 Million cell updates/sec
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simian viru
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mouse polyo
homo sapien
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9 anabaena fl
3 caenorhabdi
                                                                                                                                                                                                       homo sapien
helicoverpa
polyomaviru
mouse polyo
neurospora
drosophila
hog cholera
                                                                                                                                                                                                                                                                                                                   mycobacteri
schizosacch
aedes aegyp
schizosacch
                                                                                                                                                                                                                                                                                            saccharomyc
escherichia
   DOMAIN
REPEAT
REPEAT
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REPEAT
CARBOHYD
                                                                                                            CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
                                                                                                                                    PROPEP
                                                                                                                                                           Calcium-binding;
                                                                                                                                                                       PROSITE; PS00232; CADHERIN; Cell adhesion; Signal; Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                  TRANSMEM
                                                                                                                                                SIGNAL
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	422.7 422.7 422.7 7
	1196 282 1204 1204 1204 1204 228
ALIGNMENTS	POL_MLVAV POL_MLVCB POL_MLVFF POL_MLVFF POL_MLVFF
	P03356 P08361 P26810 P26809 P26808 P03883
	akv murine cas-br-e mu friend muri friend muri friend muri emericella

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EMBL; M76482; AAA60230.1; -.

PIR; A41088; IJHUG3.

HSSP; P09803; 1EDH.

MIM; 169615; -.

PFAM; PF00028; cadherin; 4.
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.;
"Autoantibodies against a novel epithelial cadherin in vulgaris, a disease of cell adhesion.";
                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 92069753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMAGAI M., KLAUS-KOVTUN V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i 67:869-877(1991).

FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS FILAMENTS MEDIATING CELL-CELL ADMESION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL,
                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3.
                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARCINOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s (Human),
Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM MAY BE BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation update)
KD PEMPHIGUS VULGARIS ANTIGEN) (PVA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESOPHAGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUNCTIONS.
AND INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pemphigus
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POTENTIAL.
CYTOPLASMIC (POTENT
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
DESMOGLEIN REPEAT 1
DESMOGLEIN REPEAT 1
DESMOGLEIN REPEAT 2.

21

Transmembrane; Cytoskeleton; Glycoprotein;

POTENTIAL.
DESMOGLEIN 3.
EXTRACELLULAR (POTENTIAL).

(POTENTIAL).

POTENTIAL.

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RESULT 2
GA6B_XENLA
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Best Local Similarity
Matches 15; Conserv
                                               Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       of heart precursors;

EMBO J. 16:355-568(1997).

EMBO J. 16:355-568(1997).

FOUNCTION: ASSOCIATED WITH CARDIAC SPECIFICATION AND CAN REGULATE CARDIAC-SPECIFIC TRANSCRIPTION DURING EMBRYOGENESIS. ACTIVATES THE EXPRESSION OF CARDIAC MHC-ALPHA IN VIVO.

-1- SUBCELLULAR LOCATION: NUCLEAR.

-1- SUBCELLULAR LOCATION: NUCLEAR.

-1- SIMILARITY: BELONGS TO THE GATA-TYPE TRANSCRIPTION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GA6B_XENLA
P70005;
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOVE C.D., WALMSLEY M., NIJJAR S., BERTWISTLE D., GUILLE M., PARTINGTON G., BOMFORD A., PATIENT R.; "Over-expression of GATA-6 in Xenopus embryos blocks differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoz
Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATA-6A OR GATA-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSCRIPTION FACTOR XGATA-6B (GATA BINDING FACTOR-6B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
TISSUE-LIVER;
                                                                                                                                                                                                                                EMBL; Y08865; CAA70088.1;
HSSP; P17678; 1GAU.
PFAM; PF00320; GATA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97180937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 SARTLNNRYTGPYTF 526
                                                                                                                SEQUENCE
                                                                                                                                                                   ZN_FING
                                                                                                                                                                                                        Transcription regulation;
                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                        DOMAIN
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120 ARPLNGSYGSPYT 132
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                        N
              ARTLNNRYTGPYT 14
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                                                                                                                                                                                                                     PS00344; GATA_ZN_FINGER;
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Mesobatrachia; Pipoidea; Pipidae;
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459
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107503
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260
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                                                                                                                                                                                                          FINGER; 2.
Activator;
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POTENTIAL.
POTENTIAL.
4891F6AE CRC32;
                                                   0
                                                                                                                GATA-TYPE.
GATA-TYPE.
POLY-SER.
POLY-THR.
POLY-THR.
POLY-SER.
9: 221DD428 CRC32;
                                                              Score 41; I
Pred. No. 5
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Pred. No. 7.6e-07;
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                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                 DB 1;
5.5;
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                                                                             Length 391;
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                                                     Indels
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Xenopodinae;
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                                                      Gaps
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"Genes encoding of L are located of flos-aquae.";
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   GVPF/L PROTEIN.
EMBL; U17109; AAA58714.1;
Gas vesicle.
SEQUENCE 245 AA; 28676
                                                                                                                                                                                                                                                                           MEDLINE; 97217685.
KINSMAN R., HAYES P.K.;
                                                                                                                                                                                                                                                                                                           STRAIN-CCAP
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                       Anabaena flos-aquae.
                                                                                                                                                                                             Seq. 7:97-106(1997).
FUNCTION: MAY PLAY A STRUCTURAL OR REGULATORY ROLE IN GAS
                                                                                                                                                                                     VESICLE SYNTHESIS.
                                                                                                                                                                                                                                                                                                           1403/13F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                              proteins homologous to halobacterial Gvps N. downstream of gvpC in the cyanobacterium Anal
   28676 MW;
                                                                                                                                                                                                                                                                                                                                                          Nostocales; Nostocaceae; Anabaena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
   F468D20E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
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                                                                                                                                                                                                                                                  ns N, J, K,
nabaena
                                                                                                                                                                                                                                                                     mj
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Query Match Best Local Matches 232 7 NRYTGPYTF 15 NNFTAPYTE 240 Similarity 66.7 47.6%; score 39; DB 1; Pred. No. 7.3; 1; Mismatches Ļ Length 245 0 Gaps

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HMD1\_CAEEL

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HMD1\_CAEEL STANDARD; PRT; 273 AA. 018273; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PUTATIVE HOMEOBOX PROTEIN C28A5.4. C28A5.4. STANDARD; PRT; . 273 AA

Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi

Caenorhabditis.

SEQUENCE FROM N.A. STRAIN-BRISTOL N2; PALMER S.;

Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)
-!- SIMILARITY: BELONGS TO THE DISTAL-LESS FAMILY OF HOMEOBOX PROTEINS.

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RESULT OF STANDARD ST
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Query Match
Best Local s
Matches 6
                                                                                                                                                                                                                            PARTIAL SEQUENCE, A MEDLINE; 93345448. HORST M., JENOE P., SCHERER P., MANNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _YEAST
                                                                                                                                                                                                                                                                                                                                             BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., CHURCHER C.M., CONNOR R., COPSEY TJ., DEAR S., DEVIIN K., FRASER GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAPELS K., JONES LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Hems
Eukaryota; Fangi; Ascomycota; Hems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IM44_YEAST
Q01852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX.1; 1.

PROSITE; PS50071; HOMEOBOX.2; 1.

Hypothetical protein; Homeobox; DNA-binding; DNA_BIND 102 161 HOMEOBOX.

SEQUENCE 273 AA; 30163 MW; 1665A6DF CRC33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93010953.

MAARSE A.C., BLOM J., GRIVELL L.A., MEIJER M.;
"MPII, an essential gene encoding a mitochondrial
is possibly involved in protein import into yeast
EMBO J. 11:3619-3628(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1993 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
MITOCHONDIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM44
PRECURSOR (MITOCHONDRIAL PROTEIN IMPORT PROTEIN 1) (INNER MEMBRANE
IMPORT SITE PROTEIN 45) (ISP45) (MEMBRANE IMPORT MACHINERY PROTEIN
                                                                                                                                                                                                                                                                                                             WALSH S.V., WHITEHEAD S.;
Submitted (DEC-1994) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORMPEP; C28A5.4; CE0532
PFAM; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIM44 OR MPI1 OR MIM44 OR ISP45 OR YIL022W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                               AND CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ
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Pred. No. 8.3;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                databases
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                                                                                                                                         MITOCHONDRION.
INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane protein, mitochondria.";
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                                                                                         MATRIX USING
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CO-CHAPERONE
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Query Match
Best Local
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PIR; A42548; A42548.
PIR; A42548; A42548; PFIR; A42548; PF
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P30929;
01-JUL-1993 (
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SEQUENCE
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a conceve the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictive by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and sequence analysis of the mumps virusencoding the L protein and the trailer sequence.";
Virology 188:926-930(1992).
-i- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE.
FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POSTEIN KINASE ACTIVITY.
SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA EDITING GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
-i- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
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                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mumps virus (strain Miyahara vaccine).
Viruses; ssRNA negative-strand viruses; Mononegavirales
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
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                                                                                                                                                                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 92263804.
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431 AA;
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48854 MW;
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MITOCHONDRIAL IMPORT INNER MEMBRANE
TRANSLOCASE SUBUNIT TIM44.
ATP (POTENTIAL);
002E0771 CRC32;
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Best Local
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Best Local
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                  (CRF-RB) (CRH-R2).
CRHR2 OR CRF2R.
Mus musculus (Mouse).
Eukaryota; Metazoa; Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterizations of the human parainfluenza type 2 virus gene encoding the L protein and the intergenic sequences.";
Nucleic Acids Res. 19:2739-2746(1991).
IN CION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA EDITING OF THE GENE TRANSCRIPT, AND PROTEIN OF OTHER PARAMYXOVIRUSES.
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                                                                       CRE2_MOUSE STANDARD; PRE: 431 An. 060748; Q60808; Q60748; AS Created)
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, East annotation update)
CORTICOTROPIN RELEASING FACTOR RECEPTOR 2 PRECURSOR (CRF-R) (CRF2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human parainfluenza 2 virus (strain Toshiba) (PIV-2).
Viruses: ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
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PIR; S16664; S16664.
PFAM; PF00946; Parramyx_RNA_pol; 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 2262 AA; 256380 MW; 2EF04669 CRC32;
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Sciurognathi; Muridae;
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Pred. No.
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80
       Vertebrata; Mammalia;
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EMBL; U21729; AAC52174.1; ...
EMBL; U19939; AAC52243.1; ...
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PRAM: PF00002; Tcm_2; 1.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               GCRDB; GCR_1711;
MGD; MGI:894312;
                                                              RANSMEM
                                                                                   DOMAIN
                                                                                                                                        CRANSMEM
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RECEP\_F2\_2; 1. Transmembrane; Glycoprotein; Signal.

EXTRACELLULAR (POTENTIAL)

(POTENTIAL)

(POTENTIAL).

CORTICOTROPIN

RELEASING FACTOR

5 (POTENTIAL) CYTOPLASMIC ( 4 (POTENTIAL). EXTRACELLULAR

(POTENTIAL).

(POTENTIAL)

CYTOPLASMIC EXTRACELLULAR CYTOPLASMIC

(POTENTIAL).

(POTENTIAL)

(POTENTIAL) (POTENTIAL)

CYTOPLASMIC

(POTENTIAL) (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL)

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"Identification of a novel murine receptor for corticotropin-releasing hormone expressed in the heart."; MOL. Endocrinol. 9:637-645(1995).

**NOL. ENDOCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING SHOWS HIGH-APFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR FOR CORTICOTROPIN RECEASE.

**SHOWS HIGH-APFINITY CRF BINDING. THE ACTIVITY CYCLASE.**

**MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.**

**INDICATED BY G. PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.**

**INDICATED BY G. PROTEINS HIGHLY EXPRESSED IN THE HEART. ALSO E IN LUNGS, SKELETAL MUSCLE, GASTROINTESTINAL TRACT, EPIDID IN LUNGS, SKELETAL MUSCLE, GASTROINTESTINAL TRACT, EPIDID IN LUNGS, SKELETAL MUSCLE, GASTROINTESTINAL TRACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a second corticotropin-releasing factor gene and characterization of a cDNA expressed in heart."; proc. Natl. Acad. Sci. U.S.A. 92:2969-2973(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BILEZIKJIAN L., SAWCHENKO P., VALE W.,
"Identification of a second corticotro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95166778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STENZEL P., KESTERSON R., YEUNG W., STENZEL-POORE M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96015396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A sauvagine/corticotropin-releasing factor receptor beart and skeletal muscle.";
"roc. Natl. Acad. Sci. U.S.A. 92:1108-1112/1005\"3]
                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
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01-JAN-1988
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SEQUENCE
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CARBOHYD
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P06167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEIC ACIDS Res. 15:2945-2958(1987).

-II- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS
-TO CELL RECEPTORS AND FOR INITIATING IMPECTION. NEUROMAINIDASE
ACTIVITY HELDS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING
THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING
                                                                                                                                                                                                                                                                                              EMBL; Y00114; CAA68298.1; -. EMBL; D84095; BAA12218.1; -. FIR; B27218; HNNZB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nucleotide sequence of the bovine parainfluenza genes of the F and HN glycoproteins."; Nucleic Acids Res. 15:2945-2958(1987).
                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine parainfluenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On-JAN-1988 (Rel. 06, Created)
Ol-JAN-1988 (Rel. 06, Last sequence update)
Ol-OCT-1996 (Rel. 34, Last annotation update)
HEMAGGLUTININ-NEURAMINIDASE (EC 3.2.1.18).
                                                                                                                                                                                                                                                                         Hydrolase; Hemagglutinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paramyxoviridae;
                                                                                                                                                                                                                                                      MAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO N-TERMINAL HYDROPHOBIC SEQUENCE.
SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                       NEURAMINIDASE FAMILY.
                                                        GTTRDRHSSKATN
                                                                             GIMRIRHSIGGIN 15
                                                                                                                                                                                                                                                                                     PF00423; HN;
                                                                                                    Similarity 61.8; Conservative
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SAKAI Y.,
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                                                                                                                                                             MW:
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                                                                                                   ; Score 41; DB; Pred. No. 7.3; 1; Mismatches
                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
  PRT;
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SEQUENCE FROM N.A.
MEDLINE; 86195857.
GRAY G.L., MAINZER S.E., REY M.W.,
GRAWONA C., REQUADT C.;
"Structural genes encoding the the
Bacillus stearothermophilus and Ba
J. Bacteriol. 166:635-643(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-ATCC 27811; MEDLINE; 86111694. YUUKI T., NOMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-104 FROM N.A.

SEQUENCE OF 1-104 FROM N.A.

MEDLINE; 84185455.

SIEPHENS M.A., ORTLEPP S.A., OLLINGTON J.F., MCCONNELL D.J.;

SIEPHENS M.A., ORTLEPP S.A., OLLINGTON J.F., MCCONNELL D.J.;

Nucleotide sequence of the 5' region of the Bacillus licheniformis

"Nucleotide sequence of the 5' region of the Bacillus licheniformis
alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";

J. Bacteriol. 158:369-372(1984).
                                                                                                                                                                    MACHIUS M., WIEGAND G., HUBER R.;

"Crystal structure of calcium-depleted Bacillus licheniformis alpha-
"Crystal structure of calcium-depleted Bacillus licheniformis alpha-
mylase at 2.2-A resolution.";

J. Mol. Biol. 246:545-559(1995).

-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
-IINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 30-47.

MEDLINE; 82098050.

KUHN H. FIETZEK P.P., LAMPEN J.O.;

KUHN H. FIETZEK P.P., LAMPEN J.O.;

RVHN H. FIETZEK P.P., LAMPEN J.O.;

RVHN H. FIETZEK P.P., LAMPEN J.O.;

RUHN H. FIETZEK P.P., LAMPEN J.O.;

RUHN H. FIETZEK P.P., LAMPEN J.O.;

Bactlius subtilis Enzymes.";

J. Bacteriol. 149:372-373(1982).
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01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
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                                                                                                                                                                                                                                                                                                MACHIUS M., WIEGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 89213924.

LAOIDE B.M., CHAMBLISS G.H., MCCONNELL D.J.,

"Bacillus licheniformis alpha-amylase gene,
promoter-independent catabolite repression:

J. Bacteriol. 171:2435-2442(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YUUKI T., NOMURA T., TEZUKA H., TSUBOI A TSUKAGOSHI N., UDAKA S.;
"Complete nucleotide sequence of a gene pH-stable alpha-amylase of Bacillus lich amino acid sequences of three bacterial deduced from the DNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus licheniformis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
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AMYS OR AMYL.
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d Bacillus lic
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licheniformis: compar
ial liquefying alpha.
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PIR; B24549; B24549.

PIR; A26151; A26151.

PDB; 1BPL; 17-AuG-96.

PDB; 1VJS; 12-MAR-97.

PFAM; PF00128; alpha-amylase; 1
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01-NOV-1997
01-NOV-1997
01-NOV-1997
CATALASE PREC
                                                                                                                                                                                 BROWN S.M., HOWELL M.L., VASIL M.L., ANDERSON A.J., HASSETT D.J.; "Cloning and characterization of the katB gene of Pseudomonas aeruginosa encoding a hydrogen peroxide-inducible catalase: purification of KatB, cellular localization, and demonstration that it is essential for optimal resistance to hydrogen peroxide."; Bacteriol. 177:6536-6544(1995).
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Bacteria; Proteobacteria;
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FRD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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; K01984; AAA22193.1;

; M26411; AAA22237.1;

; A17930; CAA01355.1;
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512 AA; 58549 N
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(Rel. 35, Last sequence update)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
ECURSOR (EC 1.11.1.6) (PARAQUAT INDUCIBLE CATALASE ISOZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 9
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7 -> Y (IN REF. 2).
7 -> G (IN REF. 2).
8 -> S (IN REF. 2).
9 -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                              A MEDLINE; 89296901.

A MCKINLEY-GRANT L.7. IDLER W.W., BERNSTEIN I.A., PARRY D.A.D.,
A MCKINLEY-GRANT L.7. IDLER W.W., BERNSTEIN S.R., STEINERT P.M.;
A CANNIZZARO L., CROCE C.M., HUEBBER K., LESSIN S.R., STEINERT P.M.;
A CANNIZZARO L., CROCE C.M., HUEBBER K., LESSIN S.R., STEINERT P.M.;
IT ICALIZARO L., CROCE C.M., S. 6.14848

"Characterization of a cDNA clone encoding human filaggrin and relation of the gene to chromosome region 1921.";
I consistency and selection 1921.";
I consistency and selection 1921.";
I proc. Natl. Acad. Sci. U. S.A. 86:4848 4852(1989).

C -1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES DISULFIDE-BOND FORMATION OF MAMAALIAN EPIDEMIS.

C -1- FUNCTION: SIPPARTING PROCUED AS A LARGE, INSOLUBLE, HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES CONTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
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BINDING
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILA_HUMAN STANDARD; PRT; 416 AA. P20930; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) FILAGGRIN PRECURSOR (FRAGMENT).
                                                                       MIM;
                                                                                           EMBL; M24355; AAA52454.1; PIR; A32947; A32947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fono sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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EMBL; U89384; AAB49463.1; -.
HSSP; P00432; 7CAT.
PFAM; PF00199; Catalase; 1.
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CATALASE.
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DROXIMAL HEME LIGAND (
PROXIMAL HEME CRC32;
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Pred. No.
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                          EMBL; X52841; CAA37025.1; -.

PIR; S36351; S36351.

HSSP; PG6241; IFYN.

PFAM; PF00017; SH2; 1.

PFAM; PF00018; SH3; 1.

PFAM; PF00069; PK1nase; 1.

PROSITE; PS00107; PROTEIN KINASE_ATP; 1

PROSITE; PS00119; PROTEIN KINASE_TYR; 1

PROSITE; PS50011; PROTEIN KINASE_DOM; 1

PROSITE; PS50011; SH3; 1.
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FYN_CHICK
DO5876;
Q05876;
Q05876;
Q1-FEB-1994 (Rel. 28, Created)
Q1-FEB-1994 (Rel. 28, Last sequence update)
Q1-OCT-1996 (Rel. 34, Last annotation update)
LIPID
LIPID
DOMAIN
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MOD_RES
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neural and hematopoietic Oncogene 8:823-831(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUDOL M., GREULICH H., NEWMAN L., "A novel Yes-related kinase, Yrk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WHITE LEGHORN;
MEDLINE; 93205395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neognathae;
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Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proto-oncogene; Transierase ATP-binding; Myristylation;
                                                                                                                                                                                                   Lipoprotein
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Phasianidae; Phasianinae;
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        PHOSPHORYLATION (BY PATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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SH3.
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                                                                                PROTEIN KINASE
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is expressed at elevated
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(BY
YB)
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                                                                  SIMILARITY)
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Best Local S
Matches 8
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PETERS D.J., MCGREW B.R., PEI

"In vivo phosphorylation and
oncogene product in IM-9 hum
Oncogene 5:1313-1319(1990).
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01-FEB-1994 (Re)
15-JUL-1998 (Re)
PROTO-ONCOGENE 7
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MOD_RES
SEQUENCE
                              x-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MEDIJIR; 96279837.

LEE C.H., SAKSELA K., MIRZA U.A., CHAIT E "Crystal structure of the conserved core a src family SHT domain.";

Cell 85:931-942(1996).
                                                                                                                                                                                   MUSACCHIO A., SARASTE M., WILMANNS M. "High-resolution crystal structures complexed with proline-rich peptides. Nat. Struct. Biol. 1:546-551(1994).
                                                                                                                                                                                                                                                                                                                                        "Crystal structure of the three-dimensional structur spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDILINE; 87089775.
KAWAKAMI T., PENNINGTON C.Y., ROBBINS
"ISOLATION and oncogenic potential of
"ISOLATION and oncogenic potential of
Mol. Cell. Biol. 6:4195-4201(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE: 86287278.
SEMBA K., NISHIZAWA M., 1
YAMANASHI Y., SASAKI M.,
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                                                                                                                                                                                                                                           MEDLINE; 95393198
MUSACCHIO A., SAR
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Proc. Natl. Ac
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                                                                                                                                                                                                                                                                                                                                                                                                    WIERENGA R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 93327750.
NOBLE M.E.M., MUSACCHIO A.,
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            STRUCTURE
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Nukaryota; Metazoa;
Nutheria; Primates;
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                                                                                                                                                                                                                                                                                  -RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
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8; Conservative
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Catarrhini; Hominidae;
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            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , PERRON D.C., LIPTAK L.M., LAUDA and membrane association of the human lymphoblasts.";
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Pred. No.
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PHOSPHORYLATION (BY SIMILARITY).
05970E9A CRC32;
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HIV-1 Nef
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PFAM: PF00069: pkinase: 1.

PROSITE: PS00107: PROTEIN_KINASE_ATP;

PROSITE: PS00109: PROTEIN_KINASE_TYR;

PROSITE: PS50011: PROTEIN_KINASE_DOM;

PROSITE: PS50001: SH2; 1.

PROSITE: PS50002: SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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Structure 5:1313-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Src-homology 3 domain of protein kinase p59fyn mediates binding phosphatidylinositol 3-kinase in T cells.", proc. Natl. Acad. Sci. U.S.A. 90:7366-7370(1993).
-i- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
-i- SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RENZONI D.A., PUGH D.J., SILIGARDI G., DAS P., MORTON WATERFIELD M.D., CAMPBELL I.D., LADBURY J.E.; "Structural and thermodynamic characterization of the the SH3 domain from Fyn with the proline-rich binding subunit of PI3-kinase.";
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MORTON C.J., PUGH
CAMPBELL I.D.;
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SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
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M14676; AAA36615.1;
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Myristylation;
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; Tyrosine-protein kinase; Phosphorylation;
SH3 domain; SH2 domain; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binding of the
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Best Local S
Matches 8
                                                                                                                          SEQUENCE FROM N.A.

MEDITINE: 91175680.

COOKE M.P. PERLMUTTER R.M.;

"Expression of a novel form of hematopoietic cells.";

New Biol 1:66-74(1989).
                                                                                                                                                                                                                                 FYN_MOUSE
P39688;
01-FEB-1995
01-FEB-1995
01-FCB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
NP_BIND
BINDING
ACT_SITE
MOD_RES
MOD_RES
                PALMITOYLATION.

MEDLINE: 94019312.

SHENOY-SCARIA A.M., TIMSON L.K., KWONG J., SHAW A.S., LUBLIN D.:

"Palmitylation of an amino-terminal cysteine motif of protein
tyrosine kinases p561ck and p59fyn mediates interaction with
tyrosyl-phosphatidylinositol-anchored proteins.";

Mol. Cell. Biol. "13:6385-6392(1993).
                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence upd
01-WOV-1997 (Rel. 35, Last annotation u
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
                                                                                         SEQUENCE FROM N.A.
SEE C., KIM M.G., JEG
Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
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INIT_MET
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8; Conservative
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                                                                                          , PARK D.E., PARK : EMBL/GenBank/DDBJ
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PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
SH3.

SH2.

PROTEIN KINASE.
PHOSPHORYLATION (BY PKC)
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITON.
A -> S (IN REF. 2).
A -> R (IN REF. 2).
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Pred.
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E FYN (EC 2.7.1.112) (P59-FYN).
                                                                                                                                             proto-oncogene
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SIMILARITY).
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                                                                                         S.D., SEONG databases.
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KOEGL M., ZLATKINE "Palmitoylation of terminal motif.";

E P., LEY S.

S.C., COURTNEIDGE S.A., N Src-family kinases at a

MAGEE A.I.; homologous

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72 TGTLRTRGGTGVT

8

303:749-753(1994).

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Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and for plasma membrane localization.";

J. Cell Biol. 13:1007-1015(1995).

-i. FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.

-i. CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.

-i. SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P8:
PHOSPHATIDYLINOSITOL 3-KINASE.

-i. SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-i. SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-i. SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-i. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE COMMAIN.

BELONGS TO THE SRC SUBFAMILY.
                                                          NP_BIND
BINDING
ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97345356.
WOLVEN A., OKAMURA H., ROSENBLATT Y., RESH M.D.;
"Palmitoylation of p59fyn is reversible and sufficient for plasma membrane association.";
                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol.
                                                                                                                                                                                 LIPID
                                                                                                                                                                                                                                          PFAM; PF00069; pkinase; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS50001; SH2; 1.

PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                MGD; MGI:95602; FYN.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Multiple features of the p59fyn src homology for immune-receptor tyrosine-based activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAUEN
                                                                                                                                  DOMAIN
                                                                                                                                                                                                                   ATP-binding; Myristylation;
                                                                                                                                                                                                                                                                                                                                                               L; M27266; AAA37644.1;
L; U70324; AAB09568.1;
A44991; A44991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.K.T., LINDER
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 8:1159-1173(1997).
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Е.,
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           500
                                                            MW.
                                                        PALMITATE.

SH3.

SH2.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

MW; B235E6FA CRC32;
Score 40; DB Pred. No. 10; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHAW A.S.;
                                                                                                                                                                                                                     Tyrosine-protein kinase SH3 domain; SH2 domain;
                                                                                                                                                                    BY SIMILARI MYRISTATE. PALMITATE.
                                                                                                                                                                                               SIMILARITY.
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SGTMRTRHSTGGT

Query Match Best Local S Matches 8

Similarity 8; Conserv

50.0%; llarity 61.5%; Conservative

Score 40; DB pred. No. 10; 2; Mismatches

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Length 536

Indels

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Gaps

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RESULT 11
FYN XEND
TO 11-FYN XEND
DT 01-FYN XEND
DT
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EMBL; M27502; AAA49719.1; -
PIR; A43806; A43806.
HSSP; P06241; IFYN.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
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P13406;
O1-JAN-1990
                              MOD_RES
NP_BIND
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MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
use by non-profit institutions as lo
modified and this statement is not remo
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNT: ASSOCIATES THROUGH ITS SH3 DO PHOSPHATIDYLINOSITOL 3-KINASE.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 90191723. STEELE R.E., DENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence up
01-WOV-1995 (Rel. 32, Last annotation
PROTO-ONCOGENE TYROSINE-PROTEIN KINASI
                                                                                                                                                                                                                                 LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and expression of fyn
Oncogene 5:369-376(1990).
-I- FUNCTION: IMPLICATED IN THE
-I- CATALYTIC ACTIVITY: ATP + A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed
                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                           ATP-binding; Myristylation;
                                                                                                                                                                                                                                                                        Cipoprotein.
                                                                                                                                                                                                                                                                                                                                  Proto-oncogene;
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pS50002; SH3; 1.
ncogene; Transferase;
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Anura; Mesobatrachia; Pipoidea;
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                            BY SIMILARITY.

MYRISTARE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
SH3.

SH2.

PROTEIN KINASE.
PHOSPHORYLATION (BY PKC)
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
W; 87236822 CRC32;
                                                                                                                                                                                                                                                                                                             ; Tyrosine-protein SH3 domain; SH2 do
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ea; Pipidae;
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SIMILARITY).
SIMILARITY).
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domain; Pa
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                                                       AB)
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                                                       SIMILARITY).
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RESULT 12

FYN_XIPHE

ID FYN_XIPHE

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ID FYN_XIPHE

P27446

DT 01-FEB

DT 01-FEB

DT 01-FEB

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HSSP; P06241; 1AOT.
PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
DOMAIN
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Oncogene 6:361-369(1991).
-i- FUNCTION: IMPLICATED IN THE CONTROL
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Cyprinodontiformes; Cyprinodontoidei; Poeciliidae; Xi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HANNIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RIO LANCETILLA;
MEDLINE; 91187435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xiphophorus helleri.
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservation of structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 TGTLRTRGGTGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHATIDILINOSITOL 3-KINASE.

SIMILARITY: CONTAINS 1 SH2 DOMAIN.

SIMILARITY: CONTAINS 1 SH3 DOMAIN.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES

DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN TYROSINE PHOSPHATE. SUBUNIT: ASSOCIATES THROUGH ITS SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ν
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTTILIE S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myristylation;
   Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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ture and
   Œ;
SH2.

PROTEIN KINASE.

PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3
                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
MYRISTATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine-protein kinase; Phosphorylation; SH3 domain; SH2 domain; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.;
expression
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF CELL GROWTH
TYROSINE - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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                                                                                                                                                                                  SIMILARITY).
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MA5D_SC
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Best Local S
Matches 8
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Best Local Similarity

Matches 8; Conser
                                                                                     RPB1_EUPOC
P28364;
01-DEC-1992 (
01-DEC-1992 (
15-DEC-1998 (
DNA-DIRECTED
SEQUENCE FROM N.A.
STRAIN-(68)-VIII;
MEDLINE; 93027138.
                                                                                                                                                            _EUPOC
                                           Eukaryota;
                                                        Euplotes
                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCALLON B.J., BOGITSH B.J., CARTER C.E.;

"Characterization of a large gene family in Schistosoma japonicum
that encodes an immunogenic miracidial antigen.";

Mol. Biochem. Parasitol. 33:105-112(1989).

-I- DEVELOPMENTAL STAGE: MIRACIDIA.

-I- SIMILARITY: NEARLY IDENTICAL TO IMMUNOGENIC MIRACIDIAL
ANTIGENS 81, 81 AND 8C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P13411;
01-JAN-1990
01-JAN-1990
15-JUL-1998
IMMUNOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-PHILIPPINE;
MEDLINE; 89261924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
                                                                            FRAGMENT).
                                                                                                                                                                                                                                                                                                                              Antigen;
                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                             m25214; AAA29851.1; -. en; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTLRTRGGTGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGIMRIRHSIGGI
                                                                                                                                                                                                                                                 Similarity 57:: 8; Conservative
                                         octocarinatus.
a; Alveolata; Ciliophora;
                                                                                                                                                                                                                                                                                                         120 AA;
                                                                                               (Rel. 24, Created)
(Rel. 24, Last sequence unit (Rel. 37, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIRACIDIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                        RNA POLYMERASE
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13, Created)
13, Last sequence update)
36, Last annotation update)
IDIAL ANTIGEN 5D (FRAGMENT).
                                                                                                                                                                                                                                                                                                        13541 MW;
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                                                                                                                                                                                                                                                 Score 40; DB Pred. No. 2.1; 0; Mismatches
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Pred. No.
                                                                                                                                               PRT;
                                                                                    uence update)
otation update)
LARGEST SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                        C5BE9039 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                          hypotrichs;
                                                                                                                                              478
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                                          Euplotida;
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                                                                                                                                                                                                                                                                      Length 120;
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Best Local
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15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, L
15-JUL-1999 (Rel. 38, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA(N).

SUBJUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM TEN TO TWELVE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS THE LARGEST COMPONENT OF RNA POLYMERASE II.

OMPONENT OF RNA POLYMERASE II.

SUBCELLULAR LOCATION: NUCLEAR.

INCLELLULAREOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES AR FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR TS SAND TRNA GENES.

III FOR 55 AND TRNA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN_FING
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSTRATES.
-I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Gene dosage as a possible major determinant for equal expression "Gene dosage as a possible major determinant for equal expression levels of genes encoding RNA polymerase subunits in the hypotrichous ciliate Euplotes octocarinatus.";

OCTUBER OF BURNES OF THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                             MAGGR
SCYD_MAGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X66452; CAA47068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                    MEDLINE; 95171111.
LUNDQVIST T., RICE J., HODGE C.N., BASARAB
                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SCYTALONE DEHYDRATASE (EC 4.2.1.94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                     of the rice pathogen, Magr
Structure 2:937-944(1994).
                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                                                                                                                                                                                        Magnaporthe grisea (Rice blast fungus).
Eukaryota; Fung1; Ascomycota; Euascomycetes; Pyrenomycetes;
Phyllachorales; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Nuclear protein.
ZN_FING 68 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00623; RNA_pol_A; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Repeat;
NAKASAKO M., MOTOYAMA T., KURAHASHI Y., YAMAGUCHI I., 
"Cryogenic X.ray crystal structure analysis for the complex of 
scytalone debydratase of a rice blast fungus and its tight-binding 
inhibitor, carpropamid: the structural basis of tight-binding
                                                                                   x-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                   Crystal structure of scytalone dehydratase of the rice pathogen, Magnaporthe grisea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QSGTMRTRHSTGG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S33886; S33886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAGQMVSRHKSGG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 53.17; Conservative
                                                                 98332516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478
478 AA;
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54026 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                172 AA
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                                                                                                                                                                                          PIERCE
                                                                                                                                                          disease determinant
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                                                                                                         SERRICCOCER
                                               Matches
                                                           Query Match
Best Local :
                                                                                                         Lyase; Me
SEQUENCE
                                                                                                                             -!- PATHWAY: BIOSYNTHESIS OF FUNGAL MELANIN.
-!- SUBUNIT: HOMOTRIMER.
PDB; 1STD; 19-AUG-95.
PDB; 2STD; 16-FEB-99.
                                                                                                                                                                                          Biochemistry 37:9931-9939(1998).
-!- CATALYTIC ACTIVITY: SCYTALONE = 1,3,8-TRIHYDROXYNAPHTHALENE
                                                                                                                                                                                                                 inhibition.";
4 TMRTRHSTGGT 14
|:||:| ||
80 TLRTQHFIGGT 90
                                                                                                         Melanin biosynthesis; 3D-structure.
DE 172 AA; 20250 MW; 0D93A15B CRC32;
                                              Similarity 63.7
7; Conservative
                                                           50.0%;
                                               Score 40; DB pred. No. 3.1; 2; Mismatches
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                                                                       Length 172;
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Search completed: January 7, 2000, 13:25:43

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044378 agrobacteri
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007800 mycobacteri
P74924 thermotoga
044433 drosophila
Q16926 aedes aegyp
Q22250 caenorhabdi
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## ALIGNMENTS

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Best Local
                   MALESZKA R., DE COUET H.G., MIKIC
Proc. Natl. Acad. Sci. U.S.A. 0:(
EMBL; AF01777; AAC28409.1; -.
FLYBASE; FBgn003464; sol.
PFAM; PF00648; Peptidase_C2; 1.
PFAM; PF00641; zf-RanBP; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998
01-AUG-1998
01-MAY-1999
                                                                                                                                                                                                                                   "AN ESSEA R.; YAMAMOTO M., BURNS R.G., MALESZKA R.;
"An essential cell division gene of Drosophila, absent from Saccharomyces, encodes an unusual protein with tubulin-like myosin-like peptide motifs.";
Proc. Natl. Acad. Sci. U.S.A. 94:5189-5194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96129280.

DE COUET H.G., FONG K.S., WEEDS A.G., MCLAUGHLIN P.J., MIKLOS G.L.;

"MOLECULAR and mutational analysis of a gelsolin-family member encoded by the flightless I gene of Drosophila melanogaster.";

Genetics 141:1049-1059(1995).
                                                                                                                                                                                                                                                                                                                                                      STRAIN=CANTONS;
MEDLINE; 97289742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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"A set of ordered cosmids and a detailed genetic a
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.

Mol. Microbiol. 21:77-96(1996).

EMBL; AL031514; CAA20601.1; -
SEQUENCE 421 AA; 44174 MW; 78444909 CRC32;
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Submitted (SEP-1998)
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e EMBL/GenBank/DDBJ
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Pred. No. 4.4;
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0:0-0(1998).
C6C4952E CRC32;
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Q65689;
Q1-NOV-1996
                "Human p59fyn(T) regulates OKT3-induced calcium distinct from PIP2 hydrolysis in Jurkat T cells. J. Immunol. 154:1136-1145(1995).

EMBL; S74774; AAB33113.; -
PFAM; PF00009; PHinase; 1.
PFAM; PF00017; SR3; 1.
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BREKER-KLASSEN M.M.;
Thesis (1995), Vetezinary Infectious
University of Saskatchewan, Canada.
EMBL; U31671; AAB03692.1; -
PFAM; PF00423; HN; 1
SEQUENCE 572 AA; 64668 MW; A16219
                                                                                                                                                                                                                                                                                                                                                                                                 Q16248
Q16248;
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Eukaryota; Metazoa; C
Eutheria; Primates; C
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O1-NOV-1996 (TREMBLREL.
O1-MAY-1999 (TREMBLREL.
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j. virol. 69:4308-4315(1995).
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Viruses; ssRNA negative-strand viruses;
Paramyxoviridae; Paramyxovirinae; Paramy
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01-VOV-1996
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PROTEIN_KINASE_ATP;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A16219EB CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disease
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                                                                                                                    influx by a ...";
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Best Local S
Matches 7
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MEDLINE; 97188425.
LI H.P., LIU Z.M., NIRENBERG M.;
"Kinesin-73 in the nervous system of
"Kinesin-73 in the nervous system of
Proc. Natl. Acad. Sci. U.S.A. 94:108
EMBL; U81788; AAB50404.1; -
FYYBASE; FBGN0019968; Khc-73.
FFYBGN; PF01302; CAP_GLY; 1.
PFAM; PF00225; kinesin; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOM
PROSITE; PS00845; CAP_GLY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               001349;
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 97188425.
LI H.P., LIU Z.M.,
                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etvaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence heterogeneity and polymorphic gene a Leishmania guyanensis gp63 genes."; Mol. Biochem. Parasitol. 62:173-185(1993). EMBL; L16777; AAA29239.1; ...
PFAM; PF01457: Darette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q25289;
Q25289;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                           KINESIN-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MHOM/BR/75/M4147A;
MEDLINE; 94187792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania guyanensis.
Eukaryota; Euglenozoa; Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01.NOV-1996 (TIEMBLIE1. 01, Created)
01.NOV-1996 (TIEMBLIE1. 01, Last segu)
01.NOV-1999 (TIEMBLIE1. 10, Last anno
MAJOR SURFACE GLYCOPROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
SEQUENCE
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8; Conservative
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534 AA;
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99
584 AA;
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                 KINESIN_MOTOR_DOMAIN1;
CAP_GLY; 1.
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577 N
63896 MW;
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; 60226 MW; D3941652 CRC32;
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04, Last sequence update)
10, Last annotation updat
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Pred. No. 30;
1; Mismatches
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MAJOR SURFACE GLYCOPROTEIN
; 6AA97A3E CRC32;
                                                                                                                                         stem of Drosophila embryos.";
94:1086-1091(1997).
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Pred.
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                        P90363 PRELIMINARY;
P90363;
01-MAY-1997 (TREMBLrel. 03,
01-MAY-1997 (TREMBLrel. 03,
01-AUG-1998 (TREMBLREL. 07,
GLYCOPROTEIN B (FRAGMENT).
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Best Local (
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052844;

01-NOV-1996 (TIEMBLITEL 0

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SEQUENCE
                                                                                                                                                                                                                                                              GLYCOPROTELL .
Human cytomegalovirus.
Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage;
Viruses; dsDNA viruses, cytomegalovirus.
                                                                                                                                       BINDER T., SIEGERT W.,
Submitted (AUG-1996) t
                                                                                                            EMBL;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BERLIN H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEMOTO K., SEKIMOTO M., KAGEYAMA H., FUKAMACHI K., NEMO' UEYAMA T., SENBA E., TOMITA I.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases EMBL; U35365; AAA82942.1; -
PFAM; PF00069; pkinase; 1.
PFAM; PF00017; SH2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Motor protein; Microtubules; SEQUENCE 1921 AA; 215047 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SHRSP STROKE-PRONE SPONTANEOUSLY ISSUE-WHOLE BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTO-ONCOGENE FYN.
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                                                                                              X99848; CAA68158.1;
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8; Conser
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      969
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                                                                                                                                SCHMIDT C.A.;
the EMBL/GenBank/DDBJ
      MW;
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Pred. No.
   F68398B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB Pred. No. 1e+(2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOA1DD46 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUKAMACHI K., NEMOTO
                                                                                                                                                                                                                                                                                                                                Herpesviridae
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1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPERTENSIVE
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Rattus.
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Best Local S
Matches 8
                                                                                 Query Match

Best Local Similarity

Matches 8; Conserv
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q68570 PRELIMINARY;
Q68570;
Q68570;
Q1-NOV-1996 (TrEMBLrel. 01, C:
Q1-NOV-1996 (TrEMBLrel. 01, L:
Q1-NOV-1998 (TrEMBLrel. 08, L:
GLYCOPROTEIN B (FRAGMENT).
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P90292; P90292; O1-MAY-1997 (
01-JUL-1997 (
01-AUG-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOFROLDER (GLYCOMEGALOVIRUS.)
Human Cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage;
Viruses; dsDNA viruses, Cytomegalovirus.
                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                              MEDIINE; 96365443.

LASRY S., DENY P., ASSELOT C., RAUZY M., BOUCHER J., GUYOT C.,
LEROUX M.C., LIVARTOWSKI A., REINERT P., NICOLAS J.C.,
"Interstrain variations in the cytomegalovitus (CMV) glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDER T., SIEGERT W., SCHMIDT C.A.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
EMBL; X99846; CAA68156.1; -.
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01-JUL-1997 (TIEMBLIEL 04,
01-AUG-1998 (TIEMBLIEL 07,
GLYCOPROTEIN B (FRAGMENT).
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STRAIN-BERLIN E;
                                                                                                                                                                                                                                                                                                                              gene sequence among CMV-infected children attending six day care
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-IV.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NON_TER
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                                       6
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3L; U52134; AAB53249.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTRRSTDGTN 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTRHSTGGTN 15
RTRRSTDGTN
                                     RTRHSTGGTN 15
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8; Conservative
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AA;
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                                                                                   Conservative
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                                                                                                                                                                                            9638 MW;
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7905 MW;
                                                                                                        50.0%;
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Last annotation update)
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Last annotation updat
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                                                                                 Score 40; DB 12; Pred. No. 4.3; 0; Mismatches 2
                                                                                                                                                                                                72E2051D CRC32;
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); Mismatches
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                                                                                                                           Length 83;
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Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P90392 PRELIMINARY; PRT; 170 AA. P90392; 01-MAY-1997 (TIEMBLIEL. 03, Created) 01-MAY-1997 (TIEMBLIEL. 03, Last sequence update) 01-NOV-1998 (TIEMBLIEL. 08, Last annotation update) GLYCOPROTEIN B VARIABLE REGION (FRAGMENT).
STRAIN-419-91;
MEDLINE; 96262011.
SHEPP D.H., MATCH M.E.,
PERGOLIZZI R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P89538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytomegalovirus.
Viruses; dsDNA viruses,
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-WOV-1998 (TrEMBLrel. 08, Last annotation updat
GLYCOPROTEIN B VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                             "Cytomegalovirus glycoprotein B groups associated with retinitis AIDS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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SHEPP D.H., MATCH M.E.,
PERGOLIZZI R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
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                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
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171 AA;
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19461 MW;
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Pred. No. 8.8;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPSON S.M., MILLAN C.,
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STRAIN-2515-92;
MEDLINE; 96262011.
SHEPP D.H., MATCH M.E., A
PERGOLIZZI R.;
                                                                                                                                                                                                                      P90394 PRELIMINARY; PKT; 1/2 ...
P90394;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLYCOPROTEIN B VARIABLE REGION (FRAGMENT).
                                                                                                                                                             Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHEPP D.H., MATCH M.E., LIPSON S.M., MILLAN C., PERGOLIZZI R.G.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88703; AAB48527.1; -.
NON_TER 1
NON_TER 169 169
SEQUENCE 169 AA; 19284 MW; C8D31BF5 CRC32;
                           "Cytomegalovirus glycoprotein B groups associated with retinitis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P90393 PRELIMINARY; PRT; 169 AA. P90393; ...
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLYCOPROTEIN B VARIABLE REGION (FRAGMENT).
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SHEPP D.H., MATCH M.E.,
PERGOLIZZI R.;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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||| || ||
96 RTRRSTDGTN 105
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Infect. Dis. 174:184-187(1996)
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Pred. No. 8.7;
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Search completed: January 12, 2000, 23:15:25 Job time: 188 sec

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                                           CADE_MOUSE
MURB_MYCTU
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VE6_HPV03
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AND_RHOBL
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7 rhodopseudo
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SEQUENCE FROM N.A.

AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.;

"Autoantibodies aggainst a novel epithelial cadherin in pemphigus

vulgaris, a disease of cell adhesion.";

Cell 67:869-877(1991)

-1- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE

FILAMENTS MEDIATING CELL-CELL ADHESION.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, ESOPHAGUS AND
  CHAIN
DOMAIN
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                                                                                                                                                      SIGNAL
PROPEP
                                                                                                                                                                                                                                 EMBL; M76482; AAA60230.1; ...
PIR; A41088; IJHUG3.
HISSP; P09803; 1EDH.
MIM; 169615; ...
                                                                                                                                                                                Cell adhesion; S Calcium-binding;
                                                                                                                                                                                             PFAM; PF00028; cadherin; 4.
PROSITE; PS00232; CADHERIN;
Cell adhesion; Signal; Tran;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).

(POTENTIAL).

DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3.

SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (Rel. 27, Created)
3 (Rel. 27, Last sequence update)
7 (Rel. 35, Last annotation update)
7 PRECURSOR (130 KD PEMPHIGUS VULGARIS
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POTENTIAL.
POTENTIAL.
DISMOGLEIN 3.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 3.
CADHERIN 3.
CADHERIN 4.
DESMOGLEIN REPEAT 1.
DESMOGLEIN REPEAT 2.
POTENTIAL.
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SEQUENCE
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BUXTON R.S., MAGEE A.I.;
"Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, is related to the cadherin family of cell adhesion molecules.";

Proc. Natl. Acad. Sci. U.S.A. 88:4796-4800(1991).

PROC. NATLON: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL MEMBRANE PROTEIN.

PROC. TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND ESOPHAGUS.

TONGENTAL CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
 DOMAIN
TRANSMEM
DOMAIN
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REPEAT
                                                                           SIGNAL
PROPEP
                                                                                                MIM; 125670; ...
PFAM; PF00028; cadherin; 4.
PROSITE; PS00232; CADHERIN; 2.
Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
                                                                                                                                  EMBL; X56654; CAA39976.1;
PIR; S16906; IJHUG1.
HSSP; P09803; 1EDH.
MIM; 125670; -
                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESMOGLEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSG1_HUMAN
                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91271279.
                                                                                              Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-KERATINOCYTES;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 TPMFLLSRNTGEVRT
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15; Conserv
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27, Last sequence update)
35, Last annotation update)
35, Cast annotation update)
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Catarrhini; Hominidae;
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4891F6AE CRC32;
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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
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Pred. No.
                                                       DESMOGLEIN 1.
EXTRACELLULAR (POTENTIAL).
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red. No. 3.6e-06;
Mismatches 0;
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                                      (POTENTIAL).
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Matches
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Best Local
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KOCH P.J., GOLDSON, FRANKE
01-0CT-1993 (1
01-0CT-1993 (1
01-NOV-1997 (1
DESMOGLEIN 1
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Q03763;
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TISSUS-MUZZLE EPITHELIUM;
MEDLINE; 91168965.
KOCH P.J., WALSH M.J., SCHMELZ M., GOLDSCHMIDT M.D.,
ZIMBELMANN R., FRANKE W.W.;
"Identification of desmoglein, a constitutive desmosomal
glycoprotein, as a member of the cadherin family of cell adhesion
molecules.";
                                                                                                             SEQUENCE OF 44-493 FROM N.A.
MEDLINE; 91097553.
GOODWIN L., HILL J.E., RAYNOR K., RAS
"Desmoglein shows extensive homology
                                                                                                                                                                           "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene. Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUS-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
Submitted (MAR-1991) to the 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
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(Rel. 27, Last sequence update)
(Rel. 35, Last annotation update)
1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN
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GLY/SER-RICH
POTENTIAL
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                                                                                                               RASZI L.,
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                                                                                                              MANABE M., COWIN P.; cadherin family of c
                                                                                                                                                                                                                                                                                                                                                                                                                   FRANKE W.W.;
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Best Local S
Matches 9
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DSG2_HUMAN STANDARD
Q14126;
01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
01-NOV-1997 (Rel. 35, L
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PROSITE; PS00232; CADHERIN; 2.
Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
                                                                                                                                                                                                                                 TISSUE-COLON CARCINOMA;
MEDLINE; 94192736.
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SCHAEFER
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                                                                                                                     expression catalogue
cadherins.";
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
SEQUENCE OF 777-1117 WEDLINE; 92037656.
                                                                                                                                              SCHAEFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human
expression catalogue of the desmoglein s
                                                                                                                                                                                                                                                                                                                                                            Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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BL; X57784; CAA40930.1; -.
BL; M58165; AAA62709.1; -.
R; S14603; IJBOG1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity 60.
9; Conservative
                                                                                         Res. 211:391-399(1994)
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                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
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180
496
124
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Hetazoa; Chordata; Craniata; Vertebrata; Mammalia;
Hates; Catarrhini; Hominidae; Homo.
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R (HDGC).
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POTENTIAL.

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MW; 13898584 CRC32;
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CYTOPLASMIC
CADHERIN 1.
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EXTRACELLULAR
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0.018;
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Matches 7
                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPERBENT ASPARAGINE SYNTHETASE 1).
ASN1 OR YPR145W OR P9659.3.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                          ASN1_YEAST
P49089;
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2 PMFLLSRNTGEVRT

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Similarity 50.

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Score 43; DB Pred. No. 4.8; 5; Mismatches

4.8 4.8

Indels

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Gaps

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56.6%;

PVFYLNKDTGEIYT

STANDARD

PRT;

571

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Fungi;

Ascomycota;

Hemiascomycetes;

Saccharomycetales;

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6.3.5

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TRANSMEM
DOMAIN
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SIGNAL
PROPEP
CHAIN
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polypeptide and identification of a second type of
Eur. J. Cell Biol. 55:200-208(1991).
-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (Sec or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z26317; CAA81226.1;
HSSP; P15116; INCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinf
the European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOCH P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILAMENTS MEDIATING CELL-CELL ADHESION.
SUBCELLULAR LOCATION: TYPE I MEDIATE ROTEIN (BY TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00232; CADHERIN; 3
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273
388
880
912
942
1021
1021
1111
181
308
461
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                                                     ₩.;
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POTENTIAL.
MW; 84D3B898
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DESMOGLEIN
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POTENTIAL.
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DESMOGLEIN
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DESMOGLEIN 2.
EXTRACELLULAR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WALSH M.J., ZIMBELMANN R., FI
e of the epidermal desmoglein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                           CADHERIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Signal;
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Length 1117;
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moglein precursor
desmoglein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEATS
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CARCINOMAS.
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Best Local S
Matches 8
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EMBL; U40829; A
SGD; L0002732;
                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                         ASN2_YEAST
P49090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
FAVELLO, A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZËS S.,
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
TALCH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligase: Asparagine biosynthesis; Glutamine amidotransferase; Multigene family.
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  VAN DYCK L., TETTELIN H., PURI
"An 18.3 kb DNA fragment from
unknown open reading frames, 1
                                                                                 STRAIN-S288C / FY1679;
MEDLINE; 97197982.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                              Saccharomycetaceae;
                                                                                                                                                                                                                                                                         ASN2 OR YGR124W OR G6358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00733; Asn_synthase; 1.
PROSITE; PS00443; GATASE_TYPE_II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPMFLLSR 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 52.6%: Score 40; DB Similarity 100.0%; Pred. No. 8:8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER B.; (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA88594.1; -.
AAB68284.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                 Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces
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        PURNELLE B., GOFFEAU A.;
Trom yeast chromosome VII carries four
es, the gene for an Asn synthase, remna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATASE (BY SIMILARITY); 6FA2535B CRC32;
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8.5;
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RESULT 7
CISY_MYCSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                    CISY_MYCSM
P26491;
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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VAN DYCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAN DYCK L., SKALA J., DE WERGIFOSSE P., PURNELLE B., TALL NAWROCKI A., DEL BINO S., GOFFEAU A.; SUBMILTER (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Ty and three tRNA genes.";
Yeast 13:171-176(1997).
[2]
                                                                                                                                                                                                                                           Mycobacterium smegmatis.
Mycobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteriae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae
                                                                                                 "Citrate synthase from Mycobacterium smegmatis determination and expression in Escherichia coli Biochem. J. 278:225-234(1991).
-I- CATALYTIC ACTIVITY: CITRATE + COA - ACETYL-C
                                                                                                                                                                                                           STRAIN-ATCC
                                                                                                                                                                                                                                                                                                              CITRATE SYNTHASE
                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
01-FEB-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00733; Asn_synthase; 1.
PROSITE; PS00443; GATASE_TYPE_II;
Ligase; Asparagine biosynthesis; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X83099; CAA58159.1; -. EMBL; Z72909; CAA97135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - ! - SIMILARITY: TO OTHER ASN SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: THE GATASE DOMAIN BELONGS AMIDOTRANSFERASES.
                                                                                                                                                                KUHN J
                                                                                                                                                                            DAVID M., LUBINSKY-MINK S.,
                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                          MEDLINE; 91354207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 TPMFLLSR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPMFLLSR 8
                                                                 OXALOACETATE:
ENZYME REGULATION: ALLOSTERICALLY
                           PATHWAY: TRICARBOXYLIC ACID CYCLE. SUBUNIT: HOMOHEXAMER. MISCELLANEOUS: CITRATE SYNTHASE IS
CAPABLE OF OXIDATIVE METABOLISM SIMILARITY: BELONGS TO THE CITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE PATHWAY: ASPARAGINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L0003156; ASN2.
; PF00310; GATAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                             23, Created)
23, Last sequence update)
28, Last annotation update)
(EC 4.1.3.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.6%;
100.0%;
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GATASE (BY SIMILARITY)
, 926C9736 CRC32;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 CITRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      375 AA
                                                                       INHIBITED
                                                                                                                                                                            SUISSA M., UNITZUR
 SYNTHASE
                              FOUND IN NEARLY ALL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                      ACETYL-COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 571
                                                                                                                                               Cloning, sequence
                                                                         BY NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TALLA E.,
                                                                                                                                                                                                                                                      Mycobacterium.
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ASSOCIATE AND RESOLUTION OF THE PROPERTY OF T
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NILOTJA

STANL....

D ASN1_LOTJA

STANL....

C P49092;

OT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

T 02-OCT-1996 (Rel. 34, Last annotation update)

OT 01-FEB-1996 (Rel. 34, Last annotation update)

T 02-RARGINE SYNTHETASE 1).
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                  WAILDANCE
CLARKSON D.T.;
"Molecular cloning and cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                             conditions.";
Plant Mol. Biol. 30:883-897(1996).
-!- CATALYTIC ACTIVITY: ATP + L-AS
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. GIFU / MEDLINE; 96270368
                                                                                                                                                                                                                                                                                                                                                                                                                                            euphyllophytes;
core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
 EMBL;
HSSP;
PFAM;
PFAM;
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                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                     WATERHOUSE R.N.,
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                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-C
PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE
PATHWAY: ASPARAGINE BIOSYNTHESIS.
SIMILARITY: THE GATASE DOMAIN BELONGS TO TO
                                                                                                                                                                                                         AMIDOTRANSFERASES
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PF00285; citi
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               X89409; CAA61589.1;
P17169; IGMS.
PF00310; GATASe_2;
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E; PS00480; CITRATE_SYNTHASE; 1.
Tricarboxylic acid cycle; Allosteric
Te 266 BY SIMILARITY.
TE 317 317 BY SIMILARITY.
CE 375 AA; 41501 MW; 6121D32A CRC3
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; Spermatophyta; Magnoliophyta;
Rosidae; eurosids I; Fabales;
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                                                                                                                                                                                                                                                                                                                                                      SMYTH A.J.,
                                                                                                                                                                                                                                                                                                                                                                                  B-129;
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                                                                                                                                                                                                                                                                                                           characterisation ics of asparagine
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Pred. No. 5.4;
3; Mismatches
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ophyta; eudicotyl
bales; Fabaceae;
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                                                                                                                                                                                                                                                                  L-GLUTAMINE
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tyledons;
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N-sufficient
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00443; GA
Ligase; Asparagine k
Multigene family.
INIT_MET 0
ACT_SITE 1
SEQUENCE 585 AA;
                                                                                                                                                                                                                                                     P19251; 049925; 01-NOV-1990 (Rel. 16, Created) 01-FB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) ASPARAGINE SYNTHETASE, NODULE [GLUTAMINE-HYDROLYZING] (EC 6.3. (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a copyright the EMBL between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and icentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pisum sativum (Garden pea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoid
                                                                                                                                                                                                                                                                                                                                                                                 TSAIF.Y. CORVZZI G.M.;
"Dark-induced and organ-specific expression synthetase genes in Pisum sativum.";
EMBO J. 9:323-332(1990).
PFAM; PF00310; GATASe_2; 1. PFAM; PF00733; Aen_synthase; 1. PROSITE; PS00443; GATASE_TYPE_II; Ligase; Asparagine biosynthesis; Multigene family.
                                                      EMBL; X52179; CAA36429.1;
EMBL; Y13321; CAA73762.1;
PIR; S11444; AJPMN1.
HSSP; P17169; 1GMS.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. SPARKLE;
MEDLINE; 90151604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pisum.
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                                                                                                                                                                                                          SIMILARITY: TO OTHER ASN SYNTHETASES.
                                                                                                                                                                                                                                 INDUCTION: DARK-INDUCED SIMILARITY: THE GATASE
                                                                                                                                                                                                                      AMIDOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPMFLMSR
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                 THE GATASE DOMAIN BELONGS
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66330
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GATASE (BY SIM
7FDC0436 CRC
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CRC32;
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                                                                                                                                                              restrictions
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Best Local S
Matches 7
                                             Matches
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ASN2_LOTJA
P49093;
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. These restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euphyllophytes;
core eudicots; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE 2).
                                                                                                                                                                                                EMBL; X89410;
HSSP; P17169;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. GIFU / B-129;
MEDLINE; 96270368.
WATERHOUSE R.N., SMYTH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                     SEQUENCE
                                                                                                                                      PPAM; PF00733; Asn_synthase; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Ligase; Asparagine biosynthesis; Glutamine amidotransferase;
Multigene family.
                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLARKSON D.
                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO OTHER ASN SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                            otus japonicus:
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 321
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                                                                                                                                                                                                                                                                                                                                             AMIDOTRANSFERASES.
                       TPMFLLSR 8
 TPMFLMSR 328
                                                                                                                                                                                     PF00310; GATase_2;
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                                                        Similarity
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                                                                                                                                                                                                              CAA61590.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                           and characterisation ynamics of asparagine
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                                                                                                       65838
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                                          Score 38; DB 1;
Pred. No. 20;
1; Mismatches
                                                                                                     BY SIMILARITY.
GATASE (BY SIMI
7; 2FE40574 CRC:
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20;
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CRC32;
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Query Match
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Matches 7
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CONFLICT
SEQUENCE
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ACT_SITE
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Seuphyllophytes; Spermatophy
                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00310; GATASe_2; 1.
PFAM; PF00733; Asn_synthase; 1.
PROSITE; PS00443; GATASE_TYPE_II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "TSAI F.Y., CORUZZI G.M.;
"Dark-induced and organ-specific expression of two asparagine synthetase genes in Pisum sativum.";
EMBO J. 9:323-332(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARAGINE SYNTHETASE, ROOT (GLUTAMINE-HYDROLYZING)
(GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - PATHWAY: ASPARAGINE BIOSYNTHESIS- IT TISSUE SPECIFICITY: ROOTS. - INDUCTION: DARK-INDUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - !- SIMILARITY: TO OTHER ASN SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - I - SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
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TSAI F.Y., CORUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CV. SPARKLE;
                                                                                                                                                                                                                                                                                                                                                         igase; Asparagine biosynthesis;
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Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSAI F.Y., CORUZZI G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                      65518
                            50.0%;
                                                                                                                                      ¥
Score 38; DB
Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                            BY SIMILARITY.
GATASE (BY SIMILARITY).
E -> D (IN REF. 2).
Y -> F (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                         Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 AA
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                                                     1;
                                                     Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC 6.3.5.4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration -
MBL outstation -
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321

TPMFLMSR TPMFLLSR 8

Conservative

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Indels

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Gaps

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Best Local
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         NS_BRAOL STANDARD; PRT; 585 AA.

ASNS_BRAOL STANDARD; PRT; 585 AA.

49091;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (EDEPENDENT ASPARAGINE SYNTHETASE).

Brassica oleracea (Cauliflower).

Eukaryota; Viridiplantae; Streptophyta; Embryoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE; 95148732.
LAM H.M., PENG S.S., C
                                                                                                                                                                                                                                                                                                  INIT_MET
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASNS_ARATH STANDARD; PRT; 583 AA. P49078; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) ASPARAGINE SYNTHETASE (LUTAMINE-HUDROLYZING) DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00733; Asn_synthase; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Ligase; Asparagine biosynthesis; Glu
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopeuphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO OTHER ASN SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   core eudicots; Rosidae;
Arabidopsis
                                                                                                                                                                                                                                                                                                                                        Multigene family.
                                                                                                                                                                                  321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                              ; L29083; AAA74359.1;
; P17169; 1GMS.
; PF00310; GATase_2; 1
; PF00733; Asn_synthase
                                                                                                                                                                                  TPMFLMSR 328
                                                                                                                                                                                                                                   Similarity 87. 7; Conservative
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65489
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GATASE (BY
4; F8FC9672
                                                                                                                                                                                                                                                                                                                            SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding glutamine-dependent
sis thaliana.";
a; Embryophyta; Tracheophyta; iophyta; eudicotyledons;
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CRC32;
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Best Local
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STRAIN-CV. SHO
DOWNS C.G., PO
                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. DEA; TISSUE-ROOT MERISTEM;
MEDLINE; 96158342.
CHEVALLER C., BOURGEOIS E., JUST D., RAYMOND P.;
"Metabolic regulation of asparagine synthetase gene expr
maize (zea mays L.) root tips.";
Plant J. 9:1-11(1996).
-I- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE
PYROPHOSPHATE + L-ASPARGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             core eudi
Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING]
DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00733; ASI_synthase; 1.

PROSITE; PS00443; GATARE_TYPE_II; 1.

Ligase; Asparagine biosynthesis; Glutamine amidotransferase.

INIT_MET 0 0 BY SIMILARITY.

ACT_SITE 1 1 GATASE (BY SIMILARITY).

SEQUENCE 585 AA; 65541 MW; B6DCFB50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          Zea mays (Maize).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                 -!- PATHWAY: ASPARAGINE BIOSYNTHESIS.
-!- SIMILARITY: THE GATASE DOMAIN BELONGS
AMIDOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (In) Plant Gene
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                                         -!- SIMILARITY: TO OTHER ASN SYNTHETASES
                                                                                                                                                                                                                                                                                                                                                                       Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L-GLUTAMINE PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE. PATHWAY: ASPARAGINE BIOSYNTHESIS. SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO-TANTO
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entry
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copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.
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collaboration
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Query Match
Best Local Similarity 87.8
Matches 7; Conservative
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MAIZEDB; 79071; -.

PFAM; pF00310; GATase_2; 1.

PFAM; pF00733; Asn_synthase; 1.

PROSITE; PS00443; GATASE_TYEE_II; 1.

PROSITE; PS00443; GATASE_TYEE_II; 1.

PROSITE; PS00443; GATASE_S GIUTARITY amidotransferase.

Ligase; Asparagine biosynthesis; Glutamine amidotransferase.

BY SIMILARITY).

TAAK MW; B24B0478 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORYSA
                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE; TISSUE-CALLUS;
STRAIN-CV. NIPPONBARE; TISSUE-CALLUS;
SUEYOSHI K., KAWACHI T., NAKAJIMA A., YAMAGATA H., SUGIMOTO T.,
IWASAKI T., OJI Y.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY; ATP + L-ASPARTATE + L-GLUTAMINE - AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASNS_ORYSA STANDARD; PRT; 590 AA.

Q43011;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (EC 6.3.5.4) (GLUTAMINE-
DEPENDENT ASPARAGINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                 PFAM; PF00310; GATase_2; 1.
PFAM; PF00733; Asn_synthase; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                          Ligase: Asparagine INIT_MET 0
ACT_SITE 1
                                                                                                                                                                              EMBL; U55873; AAB03991.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: TO OTHER ASN SYNTHETASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: ASPARAGINE BIOSYNTHESIS.
SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYROPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDOTRANSFERASES.
590 AA;
                                               biosynthesis; Glutamine amidotransferase
0 BY SIMILARITY.
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Pred. No. 20;
1; Mismatches
GATASE (BY SIMILARITY).
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Query Match Best Local Similarity

50.0%;

Score 38; Pred. No.

DB 1; Length 590; 21;

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Matches 7; Conservative 1; Mismatches

Oy 1 TPMFLLSR 8

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Indels

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Gaps

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321 TPMFLMSR 328

Search completed: January 7, 2000, 13:25:39 Job time: 391 sec

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Result
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Perfect score:
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333300
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score greater than or equal to the score of the result being po
and is derived by analysis of the total score distribution.
protein search, using sw model
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pir2:*
pir3:*
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$58684
H71967
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                        DNA repair and gen
H+-transporting AT
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IJHUG1
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C;Genetics:
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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993
C;Accession: A41088
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A;Cross-references:
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A; Residues: 1-999 < AMA>
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A; Reference number: A410
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Amaga1, M.; Klaus-Kovtun, V.; Stanley, Cell 67, 869-877, 1991
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Best Local S
Matches 15
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45	44	43	42	41	40	39	3 8	37	36
36	36	3 6	ω 6	36	36	36	36	36	36
47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4
1417	466	469	484	. 379	152	483	790	789	790
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T00661	H64904	A56918	149018	I49020	S36550	T06459	150178	152701	137016
hypothetical prote	hypothetical prote	farnesoid x-activa	retinoid X recepto	retinoid X recepto	E6 protein - human	62K sucrose-bindin	cadherin-6B - chic	K-cadherin - rat	cadherin-6 - human

## ALIGNMENTS

pemphigus vulgaris antigen

namun

dies against a novel epithelial A41088; MUID:92069753

cadherin in pemphigus vulgaris,

#text\_change 22-Jun-1999

J.R.

GB:M76482; NID:g190751; PIDN:AAA60230.1; PID:g190752

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F;50-615/Domain: extracellular #status predicted <EX F;52-157/Domain: cadherin repeat homology <CR1>F;160-657/Domain: cadherin repeat homology <CR2>F;270-383/Domain: cadherin repeat homology <CR3>F;390-495/Domain: cadherin repeat homology <CR3>F;390-495/Domain: cadherin repeat homology <CR4>F;616-639/Domain: cadherin repeat homology <CR5>F;616-639/Domain: transmembrane #status predicted <TF;640-999/Domain: intracellular #status predicted <IF;910-938/Domain: desmoglein repeat <DG1>F;910-938/Domain: desmoglein repeat <DG2>F;37-965/Domain: desmoglein repeat <DG2>F;310,180,545/Binding site: carbohydrate (Asn) (cova
                                                                                                                                                                                                                                           A; Map position: 18q12.1-18q12.2
C; Superfamily: cadherin; cadherin repeat homology
C; Superfamily: calcium binding; cell adhesion; duplication;
C; Keywords: calcium binding; cell adhesion; duplication;
F;1-23/Domain: signal sequence *status predicted <SIG>F;24-49/Domain: propeptide *status predicted <PRO>F;24-49/Domain: propeptide *status predicted <PRO>F;50-999/Product: desmoglein homolog *status predicted <PRO>F;50-999/Production <PRO
                                          R;Buxton, R.S.
submitted to the EMBB Data
A;Reference number: S16906
A;Accession: S16906
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type: mRNA
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l Similarity 100.0%;
l5; Conservative (
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                                                                                                                                                Library, November 1990
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Pred. No. 7.8
0; Mismatches
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7.8e-06;
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                                                                                 C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change
C;Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change
C;Accession: S14603; A38872; A37785; S38721; A48173; S24412
R;Koch, F.J.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W.
Submitted to the EMBL Data Library, March 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
A; Description: Complete sequence of the desmoglein precursor and evidence A; Reference number: $14603 A; Accession: $14603
                                                                                                                                                                                                                                               desmoglein 1 precursor - bovine
N:Alternate names: desmoglein BDGM
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A;Cross-references: GB:X56654
R;Cross-references: GB:X56654
R;Milles, L'A.; Parry, D.A.D.; Powers, E.E.; Angst, B.D.; Wagner, R.M.; Green, K.J.
J. Cell Sci. 99, 809-821, 1991
A;Title: Structural analysis and expression of human desmoglein: a cadherin-like compone
A;Reference number: A61254; MUID:92121251
A;Accession: A61254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506 R;Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ataliotis, P.; Poynter, D.; Arne Proc. Natl. Acad. Sci. U.S.A. 88, 4796-4800, 1991 A;Title: Desmosomal glycoprotein DGI, a component of intercellular desmosome A;Reference number: A39706; MUID:91271279
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A; Residues: 26-1049 <
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.;Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Arnemann, J.; Rees, D.A.; King, I.A.; Mages iochem. Soc. Trans. 19, 1060-1064, 1991
.;Title: Desmosomal 9lycoproteins I, II and III: novel members of the cadherin superfami;Reference number: A61279; MUID:92175187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Residues: 1-55
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ap position: 18q12.1-18q12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    words: calcium binding; cell adhesion; duplication; 
3/Domain: signal sequence #status predicted <SIG>
49/Domain: propeptide #status predicted <PRO>
1049/Product: desmoglein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                          206 SPMFIINRNTGEIRT 220
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85/Domain: cadherin repeat homology <CR3>
93/Domain: cadherin repeat homology <CR4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPMFLLSRNTGEVRT 15
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10; Conserv
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<WH3>
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Pred. No. 0.0013;
5; Mismatches
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hypothetical protein 6 (peff 5' region) - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 19-Mar-1997 #Bequence_revision 25-Apr-1997 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                           RESULT
S32892
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R;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. 55, 200-208, 1991
A;Title: Complete amino acid sequence of the epidermal desmoglein precursor polypepti
A;Reference number: A38872; MUID:g2037656
A;Accession: A38872
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A;Title: Identification of desmoglein, a constitutive desmosomal glycoprotein,
A;Reference number: A48173; MUID:91168965
A;Accession: A48173
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A; Molecule type: mRNA
A; Residues: 44-1043 <ZIM>
A; Residues: 44-1043 <ZIM>
A; Cross-references: EMBL:X57784; NID:g436061; PIDN:CAA40930.1; PID:g436062
A; Cross-references: EMBL:X57884; PID:g436061; PIDN:CAA40930.1; PID:g436062
A; Cross-references: EMBL:X57884; PID:g43606
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F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;180,496/Binding site: carbohydrate (Asn) (covalent) #status predicte
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A; Accession: S38721
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R;Goodwin, L; Hill, J.E.; Raynor, K.; Raszi, L.; Manabe, M.; Cowin, P.
Biochem. Biophys. Res. Commun. 173, 1224-1230, 1990
A;Title: Desmoglein shows extensive homology to the cadherin family of cell adhesion
A;Reference number: A37785; MUID:91097553
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A; Residues: 1-87;968-1043 <KO2>
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A;Residues: 44-1001,'AQPPSAT' <KO3>
A;Cross-references: GB:X57784
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A;Cross-references: GB:M58165; NID:g162966; PIDN:AAA62709.1; PID:g552318
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;Date: 13 cm.;
;Accession: S32892
;;Friedrich, M.J.; Kinsey, N.E.;
;;Friedrich, M.J.; Kinsey, N.E.;
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Best Local Similarity
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2-385/Domain: cadherin repeat homology <CR3>
2-491/Domain: cadherin repeat homology <CR4>
9-574/Domain: transmembrane #status predicted <TMA>
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ywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane
ywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane
ywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane
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A;Title: Nucleotide sequence of a 13.9kb segment of A;Reference number: S32886; MUID:93316852
A;Accession: S32892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <FRI>A;Cross references: EMBI:L08613
A;Cysperfamily: Salmonella typhimurium hypothetical
                                                                                                             citrate (si)-synthase (EC 4.1.3.7) - Mycobacterium smegmatis C;Species: Mycobacterium smegmatis C;Species: Mycobacterium smegmatis C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_cha C;Accession: S17168
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A;Residues: 1-1117 <ZIM>
A;Ross-references: EMBL:226317; NID:9416177;
R;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.;
Eur. J. Cell Biol. 55, 200-208, 1991
A;Title: Complete amino acid sequence of the e
A;Reference number: A38872; MUID:92037656
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A:Cross-references: GDB:128808; OMIM:125671
A:Map position: 18q12.1-18q12.2
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A;Reference number: S17168; MUID:91354207
A;Accession: S17168
A;Moleoule ----
                                             R;David, M.; Lubinsky-Mink, S.; Ben-Zvi, A.;
Biochem. J. 278, 225-234, 1991
A;Title: Citrate synthase from Mycobacterium
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:Residues: 777-1117
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Best Local
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20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
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Pred. No. 1.9;
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9.3;
                                                     smegmatis. Cloning, sequence determination
                                                                                            Suissa, M.; Ulitzur,
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            asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) ASN2 - yea N.Alternate names: protein G6538; protein YGR124w C; Species: Saccharomyces cerevisiae C;Date: 23-Aug-1995 #sequence_revision 19-oct-1995 #text_change 16-C;Accession: S55982; S64433 R; yan Dyck, L.; Goffeau, A. submitted to the EMBL Data Library, December 1994 A;Description: Genes for an asn synthase, a GLFG-motif nucleoporin e new ORFs, remnants—of Ty and three tRNA genes. A;Accession: S55976 A;Accession: S55976
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A;Residues: 1-375 <DAV>
A;Cross-references: EMBl
C;Genetics:
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A;Gene: gltA
C;Superfamily: citrate (si)-synthase
C;Superfamily: citrate (si)-synthase
C;Keywords: acetyl-CoA; carbon-carbon lyase; oxo-acid-lyase;
F;227,266,317/Active site: His, His, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 19 May-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
C;Accession: S52694; S69033
R;Dang, V.D.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.
submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A,Description: The sequence of S. coa,Reference number: S69019
A,Accession: S69033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) ASN1 (Alternate names: protein 9969.3; protein YPR145w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: Multiple regulatory systems control expression A; Reference number: S52694
                                                                                                                                                                             A; Map position: 16R
C; Superfamily: asparagine synthase (glutamine-hydrolyzing)
C; Keywords: asparagine biosynthesis; ligase
F; 2/Active site: Cys (amide transfer) #status predicted
                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-572 <FUL>
A;Cross_references: EMBL:U40829; NID:g1066476; PIDN:AAB68284.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Fulton
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Best Local S
Matches 7
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                                                                                               Query Match
Best Local
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Residues: 1-572 <DAN>
                                                                                                                                                                                                                                                            Cross-references: SGD:S0006349; MIPS:YPR145w
                                                                                                                                                                                                                                                                                                      Genetics:
                                                                              Matches
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347
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                                      1 TPMFLLSR 8
TPMFLLSR
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                                                                              Similarity 100
8; Conservative
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354
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                                                                              score 40; DB; pred. No. 16; 0; Mismatches
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Pred. No.
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cerevisiae cosmid
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16-Jul-1999

and

a putative

yeast (Saccharomyces

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R;Cole, S.T.; Brosch, Connor, R.; Davies,
                                                                         probable citrate synthase - Mycobacterium tuberculosis (strain H37RV)
c;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Jun-1999
C;Accession: D70539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sy Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing A; Reference number: A69250; MUID:98049343
A; Accession: F69294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA repair protein RAD25 homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Sep-1999
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A:Map position: 7R
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)
C:Keywords: asparagine biosynthesis; ligase
F:2/Active site: Cys (amide transfer) #status predicted
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A;Residues: 1-452 <KLE>
A;Cross-references: GB;AE001080;
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R:Klenk, H.P.; Clay
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A; Cross-references: EMBL: X83099; NID: g642340;
R; Van Dyck, L.; Skala, J.; de Wergifosse, P.;
submitted to the Protein Sequence Database, M:
A; Reference number: S64428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local S
Matches 8
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Best Local
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;Experimental source: strain S288C
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Residues: 1-572 <VAW>
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8; Conser
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8; Conserv
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Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                 52.6%;
72.7%;
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Pred. No. 13;
1; Mismatches
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May 1996
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                                                                                                                                                                         K; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999

A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID:99310339

A; Accession: C72756
                                              A; Experimental source: strain C; Genetics:
                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
C72756
                                                                  A;Cross-references: DDBJ:AP000058;
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                        C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision
C;Accession: C72756
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A; Residues: 1-163 <ARN>
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Science 282, 754-759, 1998
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7; Conser
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                                                                                        NID:g5103388; PIDN:BAA78949.1; PID:d1042725;
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20-Aug-1999 #text\_change 20-Aug-1999

Aeropyrum

PID:g

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A;Cross-references: GB:AE001299; GB:AE001273; NID:g3328671; A;Experimental source: serotype D, strain UW-3/Cx C;Genetics:
                                                                                                                                                                                                                                                              A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia A;Reference number: A71570; MUID:99000809
A;Accession: A71536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-393 <COL>
A;Cross-references: GB:Z95585; GB:AL123456;
A;Experimental source: strain H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A; Fulbors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987

A; Accession: D70539
                                                                                                                                                                                                                                                                                                                                                                         C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
C;Accession: A71536
                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CT260 - Chlamydia trachomatis C;Species: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.;
                      Pred. No.
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}; Mismatches
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                                             Length
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EMBO J. 9, 323-332, 1990
A;Title: Dark-induced and organ-specific expression
A;Reference number: S11443; MUID:90151604
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A;Residues: 1-583 <TSA>
A;Cross-references: EMBL:X52180; NID:g20651; PIDN:CAA36430.1; PID:g20652
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N;Alternate names: asparagine synthetase (glutamine-hydrolyzing)
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A;Title: Dark-induced and organ-specific expression
A;Reference number: S11443; MUID:90151604
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Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                        Gene: AS1
Superfamily: asparagine synthase (glutamine-hydrolyzing)
Keywords: asparagine biosynthesis; ligase
Keywords: aminator <ANN>
Fig. 175-586/Domain: Aminator <ANN-
Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: asparagine synthase (glutamine-hydrolyzing) 
Keywords: asparagine biosynthesis; ligase; 
2/Active site: Cys (amide transfer) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S11444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternate names: asparagine synthetase (glutamine-hydrolyzing) Species: Pisum sativum (garden pea)
                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X52179; NID:g20649; PIDN:CAA36429.1; PID:g20650 Comment: This protein is one of a family of glutamine amidotransferases an aminator domain, which catalyzes the ammonia-dependent reaction, and
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Residues: 1-586 <TSA>
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C; Superfamily: asparagine synthase (glutamine-hydrolyzing)
C; Keywords: asparagine biosynthesis; ligase
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A;Title: Molecular cloning and characterisation of asparagine synthetase from Lotus ja;Reference number: S69182; MUID:96270368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4)
                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X89409; NID:g897770; PIDN:CAA61589.1;
A;Experimental source: strain B-129
                                                                                                                                                                                                                                                                                                                         A; Residues:
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Best Local
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DSG1_HUMAN
DSG1_HUMAN
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                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The Use of Bioinformatics Institutions as green modified and this statement is not removed entities requires a license agreement (See or send an email to license41sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMAGAI M., KLAUS-KOYTUN V., STANLEY J.R.;

"Autoantibodies against a novel epithelial cadherin

"ulgaris, a disease of cell adhesion.";

Cell 67:869-877(1991).

-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME J

INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS A

FILAMENTS MEDIATING CELL-CELL ADHESION.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                Cell adhesion; S
Calcium-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASE: PEMPHIGUS VULGARIS (PV) IS DISEASE IN WHICH EPIDERMAL BLISTERS LOSS OF CELL-CELL ADHESION CAUSED BY AGAINST DSG3.
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97 (Rel. 35, Li
N 3 PRECURSOR
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CYTOPLASMIC (PC
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pempHiGUS VULGARIS ANTIGEN) (PVA).
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AND INTERMEDIATE
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Q14126;
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KOCH P.J., GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE KOCH P.J., GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE KOCH P.J., GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE KOCH P.J., GOLDSCHAPPER CONTROL OF GROUP OF GENERAL CHAPPE OF GENERAL PROPERTY OF COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATING CELL-CELL ADHESION.

-IS UBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARI TILSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES TESTED AND CARCINON OF TISSUES
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MEDLINE; 94192736.
SCHAEPER S., KOCH P.J., FRANKE W.W.
"Identification of the ubiquitous
expression catalogue of the desmog
                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                     Cytoskeleton;
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SIMILARITY: BELONGS
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P15116; 1NCI.
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TE; PS00232; CADHERIN; 3
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(etazoa: Chordata; Craniata; Vertebrata; Mammalia;
(imates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.5e-05;
Mismatches 0;
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ous human desmoglein, Dsg2, and
smoglein subfamily of desmosomal
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MEDLINE; 9118965.

KOCH P.J., WALSH M.J., SCHMELZ M ZIMBELKANN R., FRANKE W.W.;
"Identification of desmoglein, a glycoprotein, as a member of the molecules.";
SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
Submitted (MAR-1991) to the
                                                                                                           "Complete amino polypeptide and
                                                                                                                                REVISIONS, AND SEQUENCE OF MEDLINE; 92037656.

KOCH P.J., GOLDSCHMIDT M.D. FRANKE W.W.;
                                                                                                                                                                                                                                                        SEQUENCE OF 44-1043 FROM TISSUE-MUZZLE EPITHELIUM;
                                                                                                                                                                                   Eur. J. Cell Biol.
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                                                                                                   J. Cell Biol.
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7 (Rel. 35, Last anno
1 PRECURSOR (DESMOSO
                                                                                                                                          GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN
                                                                                                                                                                                                                                                                                                                                                            Metazoa;
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actyla; Ruminantia;
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SMOSOMAL GLYCOPROTEIN
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EMBL/GenBank/DDBJ databases.
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Pecora; Bovoidea; Bovi
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EMBL; X57784; CAA40930.1; -
EMBL; M58165; AAA62709.1; -
PIR; S14603; IJBDG1.
HSSP; P09803; 1EDH.
PFAM; PF00028; Cadherin; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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TISSUE-KERATINOCYTES;
MEDLINE; 91271279.
WHEELER G.N., PARKER A.E.,
ARNEMANN J., RUTMAN A.J.,
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                                                                        Eukaryota;
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                                                               Eukaryota; Metazoa;
Eutheria; Primates;
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TISSUE SPECIFICITY: EPIDERMIS,
DOMAIN: CALCIUM MAY BE BOUND B
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9; Conservative
                                                     (Human).
etazoa; Chordata; Craniata; Vertebrata;
imates; Catarrhini; Hominidae; Homo.
                                                                                                         PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Transmembrane;
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Pred. No. 0.17;
5; Mismatches
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MIS, MUZZLE, TONGUE AND ESOPHAGUS
ND BY THE CADHERIN-LIKE REPEATS
  S.C.
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   WATT F.M., RE
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Eukaryota; Eutheria; Bos taurus

Pecora; Bovoidea;

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HSSP; P09803; 1EDH.
MIM; 125670; -.
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Cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - !- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL
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TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND I
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
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PS00232; CADHERIN; 2.
esion; Signal; Transmembrane; Cytoskeleton;
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                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is not removed.
      Score 55; DB
Pred. No. 0.17
5; Mismatches
                                                                                                                                                      GLY/SER-RICH.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
MW; FDD79961
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CADHERIN 4.
DESMOGLEIN
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POTENTIAL.
DESMOGLEIN 1.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC
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AND INTERMEDIATE
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EMBL; M67489;
EMBL; X56966;
EMBL; X56967;
EMBL; X56968;
EMBL; X56968;
EMBL; X56968;
                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       of desmosomal glycoproteins 2 and 3 (desmocollins) in MDCK cells.";
J. Cell Sci. 96:239-248(1990).

-: FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL CELL ADHESIVENESS DIFFERENT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES.

-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-! ALTERNATIVE PRODUCTS: TWO FORMS: 1A OR DG2 (SHOWN HERE) AND 1B OR DG3; ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
-! TISSUE SPECIFICITY: EPIDERMIS AND WEAKLY IN TONGUE PAPILLAE.
-! DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE: 91239591.

MECHANIC S., RAYNOR K., HILL J
"Desmocollins form a distinct adhesion molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heterogeneous cytoplasmic domains.";

Cell Biol. 113:381-391(1991).

EQUENCE FROM No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOLTON J.L., KENNY T.P.,
SHARMA R., GARROD D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Amino acid sequence of bovine muzzle epithelial desmocollin derived from cloned cDNA: a novel subtype of desmosomal cadherins."; Differentiation 47:29-36(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 133-893 FROM N.A. TISSUE-MUZZLE EPITHELIUM; MEDLINE; 92008912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91009551.

PARRICH E.P., MARSTON J.E., MATTEY D.L., MEASURES H.R., VENNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91185414.
COLLINS J.E., LEGAN P.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Size heterogeneity,
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                                                                                                                                                                                                                                             PTM: FORM 1A IS PHOSPHORYLATED ON A SERINE BUT FORM 1B IS NOT. SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoproteins 2 and 3 (desmocollins) show N-terminal
to calcium-dependent cell-cell adhesion molecules.";
. 97:239-246(1990).
         AAA30492.1;
CAA40286.1;
CAA40287.1;
CAA40289.1;
CAA40288.1;
CAA40288.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1A), AND PARTIAL SEQUENCE
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Best Local S
Matches 7
MEDLINE: 94116981.

KING I.A., ARNEMANN J., SPURR N.K., "Cloning of the TDNA (DSC1) coding i its assignment to chromosome 18.", Genomics 18:185-194(1993).
                                                                                                                                                                                                                                                   DSC1_HUMAN
Q08554;
Q1-NOV-1997
                                                                                                                                                                                                                                                                              LT 6
LHUMAN
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CONFLICT
SEQUENCE
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SIGNAL
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REPEAT
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                                                          SEQUENCE FROM N.A.
                                                                            Submitted (JUN-1994)
                                                                                            SEQUENCE FROM N.A. TISSUE-FORESKIN;
                                                                                                                     THEIS D.G., KOCH P.J., FRANKE W.W.; "Differential synthesis of type 1 and human stratified epithelia."; Int. J. Dev. Biol. 37:101-110(1993).
                                                                                                                                                                                       Eutheria; Primates;
                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                          DESMOCOLLIN
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15-DEC-1998
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PIR; A39377; A39377
HSSP; P09803; 1EDH
                                                    TISSUE-SKIN;
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                                                                                     IMBELMANN R.;
                                                                                                                                                       EDLINE; 93283249
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: A39377;
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7; Conser
                                                                                                                                                                                               Metazoa;
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(Rel.
1A/1B
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A39377.
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                                                                                                                                                                                                                                                                     STANDARD;
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35, Last sequence update)
37, Last annotation update)
PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2/DG3).
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485
99647
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                                                                                                                                                                                                                                                                                                                                                      57.7%;
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                                                                            EMBL/GenBank/DDBJ databases
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CADHERIN 4.
CADHERIN 5.
POTENTIAL.
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MISSING (IN FORM 1B/DG3).

TN REF. 2 AND 3).
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                          for human type
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                          desmocollin
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                          and
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SEQUENCE OF 135-151 AND 283-292.
MEDLINE; 91323543.

MEDLINE; 91323543. KING I.A., MAGEE A.I

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RESULT
CAD5_PIG
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                                                                                                                                               Query Match
Best Local S
Matches 7
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CONFLICT
SEQUENCE
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CARBOHYD
VARSPLIC
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TRANSMEM
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CAD5_PIG STANDARD;
002840;
15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Keratinization is associated
                                                                                              182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDEMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERNTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERNTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERNTIAL INKED TO THE KERATINIZATION OF EPITHELIAL TISSUES. SUBCELLULAR LOCATION: TYPE I THE TISSUES. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: TWO FORMS; 1A OR DG2 (SHOWN HERE) AND 1B OR DG3; ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

TISSUE PROTEITICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH NOR AND STRONGLY STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS (POTENTIAL).
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NODE AND TONGUE
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                                                                                             FNLFYIEKDTGDI
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                                                                                                                                               Similarity 7; Conser
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resion; Glycoprotein; Transmembrane; Repeat; Signal;
.eton; Calcium-binding; Alternative splicing.
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132
100044
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ed with the expression
adherins DGII/III.";
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Pred. No.
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CADHERIN 5.
POTENTIAL.
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T -> S (IN REF. 3)
W; A287BCA9 CRC32;
                                                                                                                                                                                                                                                               POTENTIAL.
KYYLCGQDEEH -> ESIRGHTLIKN (IN
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POTENTIAL.
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                                                                                                                                                            DB 1;
6.8;
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                                                                                                                                               Gaps
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RESULT 8
CAD6\_HUMAN
ID CAD6\_HUMAN
AC P55285;
DT 01-OCT-1996

STANDARD;

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Best Local S
Matches 7
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CARBOHYD
SEQUENCE
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CARBOHYD
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Submitted (JUN-1997)
-i- FUNCTION: CADHER
                                                                                                                                                                                                                                                                                                                                        SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5).
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y13919; CAA74225.1;
HSSP; P09803; 1EDH.
PFAM; PF00028; cadherin; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                   TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
3 IFVVDKNTGDI 13
:| ||:|||:
89 VFRVDENTGDV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOUNDARIES AND PROBABLY AT CELL-MATRIX BOUNDARIES SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (JÜN-1997) to the EMBL/GenBank/DDBJ databases. FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THOSE PREFERENTIALLY INTERACT WITH THEMSETVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HEFTEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS. IT ASSOCIATES WITH ALPHA-CATENIN FORMING A LINK TO THE CYTOSKELETON
                                                7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          00028; cadherin; 5.
01049; Cadherin_C_term; 1.
PS00232; CADHERIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Cetartiodactyla; Suina; Suidae; Sus.
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: TYPE I MEMBRANE PROTEIN. FOUND AT CELL-CELL ND PROBABLY AT CELL-MATRIX BOUNDARIES (BY SIMILARITY)
                                                                                                                  87546 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            institutions as long
                                                              55.1%;
                                                                                                                                                                                                                                                            CYTOPLASMIC CADHERIN 1. CADHERIN 2.
                                                                                                                  POTENTIAL.
POTENTIAL.
1; 007F70E0
                                                              Score 43;
Pred. No.
                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                          CADHERIN
SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Transmembrane;
                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                    CADHERIN
                                                                                                                                                                                                                                                                                                                EXTRACELLULAR
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                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                CADHERIN
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                                                                                                                                                                                                                                                                                                                             VASCULAR ENDOTHELIAL-CADHERIN
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                                                           DB
13;
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                                                                                                                   CRC32;
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                                                                            Length 782;
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A SUZUKI S., SANO K., TANIHARA H.;

'A SUZUKI S., SANO K., TANIHARA H.;

'I Diversity of the cadherin family: evidence for eight new cadherins of the providence of the cadherins of the cadherins of the cadherins of the cadherins of the cadherins are calcium dependent cell adhesion proteins. C. -: FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

'C THEY PREFERENTIALLY INTERACT MITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES.

'C SORTING OF HETEROGENEOUS CELL TYPES.

'C SUBCELLULAR LOCATION: TYPE IN MEMBRANE PROTEIN.

C -: SUBCELLULAR LOCATION: TYPE IN MEMBRANE PROTEIN.

C -: TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, CEREBELLUM, AND KIDNEY. LUNG, PANCREAS, AND GASTRIC MUCOSA SHOW A WEAK EXPRESSION.

C ALSO EXPRESSED IN CERTALN LIVER AND KIDNEY CARCINOMAS.

C -: SUMLARITY: BELONGS TO THE CADHERIN FAMILY.
     CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                         REPEAT
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                               EMBL; D31784; BAA06562.1; -.
HSSP; P15116; 1NCI.
HMIN; 603007; -.
PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin_C_term; 1.
PROSITE; PS00232; CADHERIN; 3.
Cell adhesion; Glycoprotein; Phosphorylation;
                                                                                                                              REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and sequence DNA for the full coding carcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-FETAL BRAIN;
MEDLINE; 91283540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHIMOYAMA Y., GOTOH M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE, 95262134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                   REPEAT
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CADHERIN-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )6 (Rel. 34,
)8 (Rel. 37,
) PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .s (Human).
Metazoa; Chordata; Cra
^~'mates; Catarrhini; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55:2206-2211(1995).
Repeat;
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37,
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, Last annotation update)
(KIDNEY-CADHERIN) (K-CADHERIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TERASAKI
e analysis
sequence
                                                                                                                                                                                                                                                        Signal
     MW;
                            CADHERIN 1.
CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
CADHERIN 5.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
                                                                                                                                                                                                      CADHERIN-6.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; i; Hominidae; Homo.
                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., KITAJIMA M., HIROHASHI S.; of human cadherin-6 complementary and its expression in human
                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
   REF. 2).
REF. 2).
CRC32;
                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
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Query Match Best Local Similarity

54.5%;

Score 43; Pred. No.

DB 1; 13;

Length 790;

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RESULT
ID OL-CAD6
AC P152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OHTAWARA Y., SANAKA M., SUZUKI M., IGARASHI H., KIYOK. OHTAWARA Y., SHEN Q., SUGIMURA H., KINO I.;
"Isolation of complementary DNA encoding K-cadherin, cadherin preferentially expressed in fetal kidney and carcinoma.";
                                                                                CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                           PROPEP
CHAIN
DOMAIN
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-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL A THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN MANNER IN CONNECTING CELLS; CADHERINS MAY THUS C SORTING OF HETEROGENEOUS CELL TYPES.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY A-
-I- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D25290; BAA04975.1; -.
HSSP; P15116; 1NCI.
PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin, C_tern
PROSITE; PS00232; CADHERIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use. by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CADHERIN-6 PRECURSOR (KIDNEY-CADHERIN) (K-CADHERIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDH6 OR KCAD.
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                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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88340 MW;
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      54.5%;
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                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
      Score 43;
Pred. No.
                                                                                POTENTIAL.
POTENTIAL.
403CCCB3
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                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CADHERIN-6.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation;
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DB
13;
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                                                                                CRC32;
                        1;
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                        Length 789;
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N A HOMOPHILIC
CONTRIBUTE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND BRAIN
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kidney
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RESULT 10
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"Cloning and expression analysis of cadherin-10 in the CNS of the chicken embryo.",

Dev. Dyn. 209:269-285(1997).

-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTE THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORTING OF HETEROGENEOUS CELL TYPES.

SORTING OF HETEROGENEOUS CELL TYPES.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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REPEAT
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PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin_C_term;
PROSITE; PS00232; CADHERIN; 3.
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Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phas!
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15-JUL-1999
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RESULT 11
CADE_HUMAN
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SHIBATA T., SHIMOYAMA Y., GOTOH M., HIROHASHI S.;

"Identification of human cadherin-14, a novel neurally specific type
II cadherin, by protein interaction cloning.";

J. Biol. Chem. 272:5236-5240(1997).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
MANUER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES.

SORTING OF HETEROGENEOUS CELL TYPES.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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                               Calcium-binding;
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PF01049; Cadherin_C_term;
IE; PS00232; CADHERIN; 3.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 62.8 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2
INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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P53197;
              TANIHARA H., SANO K., HEIMARK R.L., ST JOHN "Cloning of five human cadherins clarifies cadherin extracellular domain and provides structurally different types of cadherin."; Cell Adhes. Commun. 2:15-26(1994).
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                      SEQUENCE FROM N.A.
                                                                                     Homo sapiens (Human)
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Eutheria; Primates; (
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Detween the Swiss Institute of Bioinformathe European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an email to 'Corsend an em
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"The H-cacherin (CDH13) gene is inactivated in human lung cancer.";
Hum. Genet. 103:96-101(1998).
-!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (E
SIMILARITY).
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EMBL; X97986; CAA66629.1; -
HSSD; P09803; 1EDH.
MGD; MGI:109173; DSC1.
PFAM; PF00028; cadherin; 5.
PROSITE; PS00232; CADHERIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
01-NOV-1997
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DESMOCOLLIN
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSC1_MOUSE
P55849;*
                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KING I.A., O'BRIEN T.J., BUXTON "Expression of the 'skin-type' d linked to the keratinization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6; T:
MEDLINE; 96420658.
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                                                                                                                                                   REPEAT
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J. Invest. Dermatol. 107:531-538(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Rodentia;
                                                                                                                                                                                                                                                                    Calcium-binding;
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CARRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERNTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERNT ISOFORMS. LINKED TO THE KERATINIZATION OF EPITHELIAL TISSUES. TO THE KERATINIZATION TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: FORMS 1A AND 1B ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
SIMILARITY:
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        Conservative
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                                                                                                                                                                                                                                                                    signal; Transmembrane; Cytoskeleton;
y; Repeat; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SKIN;
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35, Last s
36, Last a
PRECURSOR.
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                      Alternative POTENTIA
DESMOCCILIN 1A/1B.

EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CADHERIN 1.

CADHERIN 2.

CADHERIN 3.

CADHERIN 5.

POTENTIAL.

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desmosomal cadherin
f epithelial tissues
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        18)
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Best Local
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MEDLINE; 95249541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 95073006.
TANIHARA H., SANO K., HE
"Cloning of five human c
cadherin extracellular d
structurally different t
Cell Adhes. Commun. 2:15
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SEQUENCE
                                                                                                                                                      EMBL; L34057;
EMBL; L33477;
HSSP; P09803;
MIM; 600562; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT 1996 (Rel. 34, Created)
01-0CT 1996 (Rel. 34, Last sequence upd
01-NOV-1997 (Rel. 35, Last annotation u
BRAIN-CADHERIN PRECURSOR (BR-CADHERIN)
(CADHERIN, NEURAL TYPE, 2).
      SIGNAL
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCALITY: BRAIN.
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P55289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                         Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed cadherin
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                                                                                                                                                                                                                                                                                                                                                                                EXPRESSED CADHERIN PSEUDOGENES ARE LOCALIZED to the the spinal muscular atrophy gene."; or Natl. Acad. Sci. U.S.A. 92:3702-3706(1995).
FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL A THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN MANUER IN CONNECTING CELLS; CACHERINS MAY THUS C SORTING OF HETEROGENEOUS CELL TYPES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: BRAIN.
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                                                                                     PF00028; cadherin; 5.
PF01049; Cadherin_C_te;
TE; PS00232; CADHERIN; ;
adhesion; Glycoprotein;
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6; Conser
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AAB48539.1;
LEDH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ... ST JOHN T., SUZUKI S.;
...unerins clarifies characteristic fea
ferent domain and provides further evidence
ferent types of cadherin.";
n. 2:15-26(1994).
                                                                        Repeat;
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Catarrhini; Hominidae;
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        POTENTIAL.
POTENTIAL.
BRAIN-CADHERIN.
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21;
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090763 gallus gall
055701 synechocyst
076356 caenorhabdi
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Mus.
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095151 homo sapien
p91388 caenorhabdi
065875 pisum sativ
Q63418 rattus norv
Q84181 human papil
Q9ykd6 tomato mosa
09z9u5 bacillus sp
027477 methanobact
P95585 rickettsia
p95659 rickettsia
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Matches 8
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Matches
                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
EMBL: D64000; BAA10231.1; -.
                                                                                                                                                                                                                                                                                                                                                                             KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAK
MIYALIMA N., HIROSAWA M., SUGJURA M., SASAMOTO S., KIMURA
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGIURA M., TABATA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
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PFAM; PF01049; Cadherin_C_term; 1.

PROSITE; PS00232; CADHERIN; 3.

Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat.

SEQUENCE 785 AA; 87171 MW; F27A6881 CRC32;
                                                                                                                                                                                                 EMBL; D64000; BAA10231.1;
Hypothetical protein.
SEQUENCE 214 AA; 24539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TABATA S.
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EMBL; D42150; BAA07721.1;
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Similarity 66.7%;
8; Conservative
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Similarity 42.9%;
6; Conservative
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09, Last annotation update)
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Pred. No. 1.7;
4; Mismatches
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ARUO K., OKUMURA S.,
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Best Local Similarity 72.'
Matches 8; Conservative
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01-NOV-1998 (TREMBLIEL 0
01-NOV-1998 (TREMBLIEL 0
01-MAY 1999 (TREMBLIEL 1
PARAXIAL PROTOCADHERIN.
                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: TYPE EMBL; AF067611; AAC19184.1; -. PFAM; PF00028; cadherin; 3. PROSITE; PS00232; CADHERIN; 1. Cell adhesion; Glycoprotein; TSEQUENCE 1329 AA; 146518 MW
Neopterygii;
Cyprinoidea;
[1]
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUUDERS D., SHOWNKEEN S
SNALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                               1288
             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazon; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Gtariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                                                                                           093508
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"The sequence of C. e
Submitted (JUN-1998)
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Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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01-NOV-1998 (TrEMBLrel.
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C45G7.6 PROTEIN.
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Rhabditidae; Peloderinae; Caenorhabditi

    Transmembrane; Calcium-binding;
    MW; B161D39E CRC32;

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C STRAIN-WHITE LEGIORN; TISSUE-BRAIN;

X MEDILINE; 95309115.

X MARAGAWA S., TAKEICHI M.;

A NAKAGAWA S., TAKEICHI M.;

I "Neural crest cell-cell adhesion controlled by sequential and "Neural crest cell-cell adhesion of novel cadherins.";

L Development 121:1321-1332(1995).

C -! - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY R EMBL; D42149; BAA07720.1; -

R PFAM; PF00028; cadherin; 5.

R PFAM; PF01049; Cadherin; 5.

R PFAM; PF01049; Cadherin; 3.

R PFAM; PF01049; Cadherin; 3.

R PFAM; PF01049; Cadherin; 3.

Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Rep Celladhesion; Glycoprotein; Transmembrane; Calcium-binding; Rep Celladhesion; Glycoprotein; Transmembrane; Calcium-binding; Rep
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01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                        Homo sapiens (Human).
Eukaryota; Metazoa; (
Eutheria; Primates; (
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Genomics 0:0-0(1998).
               SEQUENCE FROM N.A.
YOSHIDA K., YOSHITOMO-NAKAGAWA
                                                                                                                                                                                                                                                                                                                                                              Neognathae;
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                                        Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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TYPE
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                                                 Mammalia;
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SIMILARITY)
                SUGANO
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                                                                                                                                                                                        0
                                                                                                                                                                                                                                         Repeat
                                                                                                                                                                                        Gaps
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Query Match
Best Local Similarity
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RESULT
060246
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Best Local S
Matches 7
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Best Local S
Matches 7
Genomics 0:0-0(1998)

1- SUBCELULAR LOCATION: TYPE EMBL; ABOOCTST; BARASIG6.1; --
PFAM; PF00028; cadherin; 5.
PROSITE; PS00232; CADHERIN; 5.
Cell adhesion; Glycoprotein; TriseQuence 1200, AA; 130337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOSHIDA K., YOSHITOMO-NAKAGAWA K., SEKI N. Genomics 0:0-0(1998).
-1-SUBCELLULAR LOCATION: TYPE I MEMBRANE EMBL; AB006756; BAA25195.1; -. PFAM; PF00028; cadherin; 6. PROSITE; PS00232; CADHERIN; 6. Cell adheston; Glycoprotein; Transmembrane SEQUENCE 1072 AA; 116463 MW; A3DF367C
                                                                                                                                                                                                                                                        PCDH/ (P. PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PCDH/ PC
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060247;
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PFAM; PF00028; cadherin; 6.
PROSITE; PS00232; CADHERIN; 6
Cell adhesion; Glycoprotein;
SEQUENCE 1069 AA; 116104 N
                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-MAY-1999 (TrEMBLrel. 10,
PCDH7 (BH-PCDH)B.
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                                                                                                                                                                                                      YOSHIDA K.,
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Similarity 58.3%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                   YOSHITOMO-NAKAGAWA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                 TYPE
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Transmembrane; Calcium-binding; Repeat.
MW; F1732B30 CRC32;
     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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Last annotation updat
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Pred. No. 75;
3; Mismatches
  Transmembrane; Calcium-binding; MW; 56F1CD33 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Calcium-binding; W; A3DF367C CRC32;
                                                                                                                                                 I MEMBRANE
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                                                                                                                                                                                                                                                                                         Vertebrata; Mammalia;
ae; Homo.
                                                                                                                                                 PROTEIN
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53.8%; 58.3%;

Score Pred.

N 42

85;

4

Length

3;

7; Conservative

Matches

||| :| ::||| 533 GIFAIDPDSGDI 544

2 GIFVVDKNTGDI 13

ô g 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10,

DACHSOUS

PRELIMINARY;

024292;

024292

RESULT 10 024292

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Gaps
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SEQUENCE 4307 AA; 478958 MW; 3486FC46 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KERLAYNGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RIRKNESS E.F., DOUGHERY B.A., MCKENNEY K., ADAMS M.D., LOFFUS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., 2HOU OVERSEEK R., GOCATNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                  AINSCOUGH R.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                       Caenorhabditis elegans,
Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Rhabditida,
Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (Tremblrel. 05, Created)
01-JAN-1998 (Tremblrel. 05, Last sequence update)
01-ANG-1999 (Tremblrel. 11, Last annotation update)
01-AUG-1999 (Tremblrel. 11, Last annotation update)
(EC 1.2.7.-) (AOR-3).
AF0340.
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Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 41; DB 5; Length 43072.7%; Pred. No. 5.1e+02;
Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
                                                                         Last sequence update)
Last annotation update)
                  4307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 AA.
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-1- SUBUNIT: HOMODIMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN*VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
                                                         Created)
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                                                                                                                                                                                                                                                                                                                              CAA84721.1; JOINED.
CAA84721.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                         CAA84661.1; JOINED.
CAA84661.1; JOINED.
CAA84339.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CAA84339.1; JOINED ; CAA84339.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00028; cadherin; 6.
PROSITE; PS00232; CADHERIN; 9.
                                  019319; 019785; 021606;
01-NOV-1996 (TEMBLEL 01,
01-MAY-1999 (TEMBLEL 10,
01-MAY-1999 (TEMBLEL 10,
                                                                                                                                                                                                                                                                                                                                                                         CAA84661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                F25F2.2 PROTEIN.
F25F2.2.
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029907
019319
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                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 95324813.

CLARK H.F., BRENTRUP D., SCHNEITZ K., BIEBER A., GOODWAN C., NOLL M.;
"Dachsous encodes a member of the cadherin superfamily that controls imaginal disc morphogenesis in Drosophila.";
Genes Dev. 9:1530-1542(1995).
-: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat.
SEQUENCE 3380 AA; 366356 MW; 7D83FAC3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heliothis armigera entomopoxvirus (HaEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.8%; Score 42; DB 5; Length 3380; Best Local Similarity 58.3%; Pred. No. 2.7e+02; Matches 7; Conservative 4; Mismatches 1; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
  5
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J. Gen. Virol. 0:0-0(1997).
EEMBL. AF017791; AAB966621.
SEQUENCE 148 AA; 17488 NW; A945DB09 CRC32;
                                                                                                                                                                             3380 AA
    Mismatches
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EMBL, L08811; AAA79329.1; FLYBASE; FB900000497; ds. PFAM; PF00028; cadherin; 25. PROSITE; PS00232; CADHERIN; 18.

SEQUENCE FROM N.A

PRELIMINARY;

037171

RESULT 11 037171

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2 GIFVVDKNTGDI 13

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Best Local Similarity Matches 8; Conserv

Query Match

SEQUENCE FROM N.A.

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RESULT
Q63315
ID Q6
AC Q6
DT Q1
                                                                                                                                               Query Match
Best Local Similarity
Whiches 7; Conserve
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DOMAIN
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL SEQUENCE
                                                                                                                                                                                                                                                                                        BAECKMAN M., KAELLSTROEM H., JONSSON A.B.;
"The phase-variable pilus-associated protein PilC is commexpressed in clinical isolates of Neisseria gonorrhoeae,
Q63315 PRELIMINARY;
Q63315;
Q1-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                           sequence variability among stra. Microbiology 144:149-156(1998). EMBL; AJ001121; CAA04547.1; SEQUENCE 1033 AA; 112936 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical Multigene fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF01314; AFOR; 1.
                                                                                                                                                                                                                                                                                                                    MEDLINE; 98129088.
BAECKMAN M., KAELLSTROEM H.,
                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              033373
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1-JAN-1998 (TrEMBLrel.
1-AUG-1998 (TrEMBLrel.
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DOMAINS II AND III SURROUND THE OPPOSITE SURFACE OF THE TUNGSTEN

COFACTOR AND ARE INVOLVED IN INTERACTIONS WITH THE DIFFERENT

METAL CENTURES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE AOR/FOR/GAPOR/CAR/HVOR FAMILY.

L; AED01081; AAB90895.1; -.

R; AF0340 -
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                                                                                                                             1 FGIFVVDKNTGDINI 15
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                                                                                                    YGIFDDDKGTGTVKV 818
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                              PRELIMINARY;
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413
598
291
294
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                                                                                                                                                                                                                                                                                                                                                                                             beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                             strains.
                                                                                                                                                            Score 40; DB
Pred. No. 1.6e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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DOMAIN II.
DOMAIN III.
IRON-SULFUR
IRON-SULFUR
 Created)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                               PRT;
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                               813
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1.6e+02;
5;
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86;
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R (BY SIMILARITY).
R (BY SIMILARITY).
R (BY SIMILARITY).
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Matches 7
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01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                          SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
                                                                                                                                                                                                                  STRAIN-WISTAR;
                                                                                                                                                     Molecular cloning and characterization of the cadherin family, PB-cadherin."; Biol. Chem. 271:11548-11556(1996).
                                                                                                                                                                                    MATSUMOTO K., NAKAMURA
                                                                                                                                                                                                        EDLINE;
106
                  3 IFVVDKNTGDIN 14
                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                                                                                                                                          TYPE PB-CADHERIN
IFLIDELTGDIH
                                     similarity 58.:
7; Conservative
                                                                                                                                                                                              K., HONDA S.,
                                                                                                                                                                                                                 TISSUE-BRAIN;
117
                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                              51.3%;
                                                                                                                                                                                               YAMAMOTO T.,
                                                                                                                                                                                                                                                                                    01, Last sequence update)
10, Last annotation update)
                                     Score 40; DB 11;
Pred. No. 1.2e+02;
4; Mismatches 1
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                                                                                                                                                                           of a
                                                                                                                                                 PROTEIN
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                                                        Length 813,
                                                                                                                                                (BY SIMILARITY).
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Rattus.
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Fitle: Perfect s Sequence:

score:

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed s derived by analysis of the total score distribution.
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Pemphigus foliaceu
Rat protocadherin
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Matches 15
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27-NOV-1991; US-798918.

(USSH) US DEPT HEALTH & HUMAN SERVICE.

A MENGAI M, Klaus-kovtun V, Stanley JR;

WPJ; 93-067436/08.

WPSDB; 035992.

DNA encoding pemphigus vulgaris antigen - useful in protein the protein of the pemphigus vulgaris and the protein the sequence is the pemphigus vulgaris 130kD antigen. The sequence is the pemphigus vulgaris 130kD antigen. The sequence is the pemphigus vulgaris and tree adhesion molecule.

Sequence 999 AA;
                                                                                                                                                                                                                                                                                                                                  23-JUL-1996.
30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44444
rused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing suprabasal, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
US7798918-A.
15-DEC-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1997 (first entry)
Pemphigus vulgaris antigen
Autoantibody; immunoglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
J08188540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1993 (first entry)
Human pemphigus vulgaris 130kD antigen.
Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein; cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermatology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment;
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immunoglobulin G; IgGl; fusion protein; di
mphigus vulgaris; PV; bulla; blister; skin
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                                                                                                                                                                                                                                                                                                                      Premphigus vulgaris auto-antigens and multiple sclerosis non-self pri antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in auto-immune disease

Claim 1: Page 40; 58pp; English.

Claim 1: Page 40; 58pp; English.

Chaim 2: Pharmaceutical preparations for tolerisation to antigens comprise ceither an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is derived from the human desmoglein a protein (amino acids 260-220) and is implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein protein are described in W04841-47.
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Sequence
                          W64816 standard; peptide; 15 AA.
W64816;
W55EP-1998 (first entry)
Desmoglein-3 206-220.
Desmoglein: DG; gene therapy; pemphigus vulgaris; microparticle; autoantigen; autoimmune disease; MHC.
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07-MAR-1996; U03182.
07-MAR-1995; US-400796.
(HARD ) HARVARD COLLEGE.
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WO9627387-A1.
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Pred. No.
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PI Curley JM, Hedley ML, Langer RS;

PI Curley JM, Hedley ML, Langer RS;

PR WPI; 98-427077/36.

PT Microparticle encapsulated nucleic acids - for recombinant with perpension of proteins e.g. in gene therapy

PT expression of proteins e.g. in gene therapy

PS Disclosure; Column 4; 42pp; English.

CC comprising a polymeric matrix and a nucleic acid. The polymeric comprising a polymeric matrix and a nucleic acid. The polymeric comprising a polymeric matrix and a nucleic polymers having a solubility comprising a polymeric matrix consists of one or more synthetic polymers having a solubility comprising a polymeric matrix consists of one or more synthetic polymers having a solubility comprising a polymeric matrix consists of the microparticles have a diameter of less than 10 more membodiment the microparticles are coloum from includes an expression control sequence conservatively linked to a coding sequence, where the expression product cof the coding sequence is a polypeptide having a length and a sequence compression product is thus an effective stimulator of an immune compressed by the nucleic acid. It is associated with pemphigus the control captic portion of the processed by the nucleic acid. It is associated with pemphigus
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Matches 15
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06-JAN-1998;
22-JAN-1997;
A microparticle preparation (MP) has been developed, consisting of microparticles having a diameter of less than 100 mu m. The MP comprises:
(a) a polymeric matrix (PM) consisting of one or more synthetic polymers having a solubility in water of less that 1 mg/l; and (b) an expression vector selected from RNA molecules (at least 50% of which are closed circles) or circular plasmid DNA (at least 50% of which are supercoiled). Also described is a MP of at most 20 microns in diameter, comprising; (a) a PM; and (b) a NAM comprising an expression control sequence operatively linked to a coding sequence, where the coding sequence encodes an expression product selected from: (1) a polypeptide at least 7 amino acids in length, having a sequence identical to the sequence of: (1) a fragment of a naturally-occurring mammalian protein; or (ii) a fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1998.
22-JAN-1997;
22-JAN-1997;
                                                                                                                                                                                                                                                    gene therapy
                                                                                                                                                                                                                                                                         matrix and nucleic
                                                                                                                                                                                                                                                                                         WPI; 98-427556/36
New preparations
                                                                                                                                                                                                                                                                                                               Curley JM, Hedley ML, Langer WPI; 98-427556/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                  Disclosure; Page 8; 101pp; English
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associated peptide; pathogen; gene therapy; genetic disease;
n; downregulation; immune response.
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US-787547.
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                                                                                                                                                                                                                                                                       of microparticles - comprising a synthetic polymer ic acid comprising an expression vector for use in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  through the hinge region used to treat pemphigus foliaceus claim 1; Page 10-12; 17pp; Japanese.
This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein for detecting pemphigus foliaceus antibodies which is also useful for detecting pemphigus foliaceus antibodies which is useful in immunodiagnosis. The fusion protein has little or no side effect
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R86867 standard; Protein; R86867; Cirst entry) Rat protocadherin pc5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pemphigus foliaceus antigen-IgG constant region fusion protein through the hinge region used to treat pemphigus foliaceus
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Sequence 15 AA;
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CC 88085-886867 represent the sequences for three protocadherins. This pc sequence represents the rat protocadherin pc5. These sequences are related to cadherin, and possess cell adhesive ability. Cadherins are composed of an N-terminal extracellular domain cadherins are composed of an N-terminal extracellular domain control of the consists of 5 unique subdomains, a membrane spanning domain, and a composed of an N-terminal extracellular domain cytoplasmic domain interacts with the cytoplasmic domain interacts with the cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the cadherins adhesive function. The cytoplasmic domain is not present in all cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to the cadherins which do not possess a cytoplasmic domain appear to protocadherins and interacts and a different method from those with a cytoplasmic domain.

CC These sequences were isolated using primers i and 2 (see T03575 and constitution) and the cell cell cell cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these constitutions and can be used therapeutically.
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27-FEB-1997.
23-AUG-1995; 031033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW, Schaefer S;
WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                                      W13009; w13009; (first entry)
21-NOV-1997 (first entry)
Segment of desmosomal cadherin, desmoglein Dsg2, cell; surface; epithelial; Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; carcinoma; desmosome; antibody; epitope; targetted delivery;
directed against epitopes of the present sequence can be used to diagnose, i.e. the detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods as a therapeutic to deliver agents, e.g. other Ab or toxins, to
                                                                                                Antibody reactive with part of desmosomal cadherin exposed on surface of epithelial or carcinoma cells, not bound to desmosomes useful for diagnosis and treatment of carcinoma micrometastases Claim 7; Page 5; 8pp; German.

The present sequence is a segment of the desmosomal cadherin (DC) desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab)
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Sequence 616 AA;
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N-PSDB; T03574.
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27-JUN-1994; US-268161
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P 23-AUG-1995; 031033.

R 23-AUG-1995; DE-031033.

R 23-AUG-1995; DE-031033.

R (PROG-) PROCEN BIOTECHNIK GMBH.

P Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, useful for diagnosis and treatment of carcinoma micrometastases of Claim 9; Page 5; 8pp; German.

C The present sequence is a segment of the desmosomal cadherin (DC), desmoglein Dsg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab)
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Sequence 263 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithe carcinoma; desmosome; antibody; epitope; diagnosis; detectio micrometastasis; separation; enrichment; targetted delivery;
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                    Streptococcus pneumoniae protein; genetic immunisation; antagonist; immunological response; inoculation; antibody production; inhibitor; T cell immune response; antimicrobial compound; bacterial adhesion; extracellular matrix protein; protein-mediated cell invasion; wound;
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; Dsg2; cell; surface; epithelial;
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CT This represents a Streptococcus pneumoniae protein that is a possible contion transporting ATPase, and is encoded by a DNA of the invention. CT The DNA sequences were isolated from Streptococcus pneumoniae strain CC 0100933 (NCIMB 40794). The Streptococcus pneumoniae proteins of the CC invention can be used to identify compounds which interact with and CC inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins, through genetic climunisation. They can also be used to induce an immunological response in a mammal by inoculation with the S. pneumoniae proteins or delivery cof the encoding nucleic acids in a vector adequate to produce antibody and/or T cell immune responses to protect the animal from disease. The CC proteins can also be used to identify antimicrobial compounds which are capable of inhibiting their bioactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian cell invention of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.

Sequence 249 AA;
                        20-NOV-199/.
14-MAY-1997; U07950.
14-MAY-1996; US-017670.
16-MAY-1996; US-017670.
16-MAY-1997; U07950.
16-MAY-1997; U07950.
16-MAY-1997; U07950.
16-MAY-1997; U07950.
16-MAY-1996; US-017670.
16-MAY-19970.
16-MAY-1996; US-017670.
16-MAY-1996; US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Streptococcus pneumoniae proteins and rediagnosing anti-microbial agents for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae WO9743303-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 296; 483pp; English
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Matches Query Matc Best Local 201 TIQYLLSANTAEVLT 1 TPMFLLSRNTGEVRT 15 Similarity
9; Conser Conservative 51.3%; Score 39; DB Pred. No. 11; Mismatches 1; ű Indels 0 Gaps

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W80699

**v**80699 standard; **Protein**; 835

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24-DEC-1998 (first entry)

5. pneumoniae cation transporting ATPase.

Streptococcus pneumoniae protein; recombinant; gene expression; DNA

virulence; antibody; infection; detection; treatment; hypothetical;

cell wall biosynthetic, external target; minimal gene set protein.

chip;

STOCOCCUS pneumoniae

13-DEC-1996; US-036281.

(ELIL ) LILLY & CO ELI Baltz RH, Burgett SG, I Mills BJ, Norris FH, Po Skatrud PL, Smith MC, ( Dehoff BS, Hoskins JA, Jaskunas Peery RB, Rockey PK, Rosteck PR, Solenberg PJ, Treadway PJ,

SR

Peery RB, Rocke , Solenberg PJ,

Young ; ; 98-348529/30.

N-PSDB; V65261.

Streptococcus pneumoniae nucleic acid for evaluating gene expression, and ic id sequences - v used in DNA chips n of virulence

genes Claim 3;

Claim 3; Pages 288-291; 333pp; English.
This sequence represents a Streptococcus pneumoniae cation transporting ATPase. The invention provides DNA sequences (V65201 to V65304) from the Streptococcus pneumoniae genome and corresponding protein sequences

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Best Local
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See also
Sequence
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02-MAY-1990;
03-MAY-1989;
26-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell wall biosynthetic, external target, or minimal gene set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat
                                                         The pro
                                                                           Disclosure; Fig 2A; 91pp; English.

The DNA sequence encoding this protein was isolated from clones selected from a pea nodule cDNA library from the variety of P.sativum. Human AS cDNA was used as a probe-
                                                                                                                                                                                                                                                                                                                                                                                                                             Pisum
                             coding sequence. Recombinant AS can be used to engineer herbicinesistance, as a dominant selectable marker, to select novel herbicides or compounds useful for synchronising plant cells in
                                                                                                                                                          (UYRO-) ROCKFELLER UNIV
Coruzzi GM, Tsai FY;
WPI; 90-361471/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Asparagine synthetase ASI. asparagine synthetase; transgenic plant; herbicide resistance; drought tolerance; nitrogen fixation; pea.
                                                                                                                           transgenic plants
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                                                                   protein is produced by expression vectors containing the AS1
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586 A/
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US-514816.
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Pred. No.
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Query Match Best Local

Similarity

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transgenic plants

Disclosure; Fig 2B; 91pp; English.

The DNA sequence encoding this protein was isolated from cDNA clones selected from a pea nodule cDNA library from the "Sparkle" variety of P.sativum. Pea ASI CDNA was used as a probe.

The protein is produced by expression vectors containing the AS2 coding sequence. Recombinant AS can be used to engineer herbicide resistance, as a dominant selectable marker, to select novel in the AS2 coding sequence as a dominant selectable marker, to select novel to several sections or compounds useful for synchronising plant cells in
23-JUN-1988; 02129.
24-JUN-1987; US-66078.
(WHIT-) Whitehead Inst.
Fink GR, Trueheart J, El
WPI; 89-023850/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1990; US-5148
(UYRO-) ROCKFELLER U
COTUZZI GM, TSAI FY;
WPI; 90-361471/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A comparison of pea AS and human AS polypeptides reveals an overall homology of 47% at the amino acid level, c.f. 86% between AS1 and AS2. There are several serious of high local homology (greater than 80%) shared between the pea AS and human AS polypeptides. See also Q06598, Q06622 and Q06623.
                                                                                                                                           02-JUL-1990 (first entry)
ORF incorporated within the HIS4
Yeast promoter; yeast pheromones;
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                                                                                                          Saccharomyces
WO8810308-A.
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03-MAY-1989;
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US-514816.
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                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis Claim 5; Page 32; 181pp; English.

The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid. Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1997; U21976.
27-NOV-1996; US-031879.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO, Reid RH, Zarfos PN;
WPI; 98-322654/28.
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Claim 5; Fig 4; 5lpp; English.
CRF iles between the FUS 1 or BIK 1 promoter, BIK 1 running 3' to 5'.
At least one polypeptide may be promoted within a high-copy vector induced by a-factor for alpha cells, alpha-factor for a-cells using this promoter system.
Sequence 407 AA;
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Streptococcus pneumoniae polypeptide.
Polypeptide; ORF; open reading frame; infection; bacterial;
Streptococcal; bacteremia; diagnosis; prophylaxis
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New DNA fragment contg. protein encoding gene and yeast promoter controlled by mating pheromone allowing efficient and
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Best Local S
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Best Local S
Matches 8
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009661;

01-NOV-1996 (TIEMBLITEL 01, Crea

01-NOV-1996 (TIEMBLITEL 01, Last

T 01-MAY-1999 (TIEMBLITEL 10, Last

""""""" 137.7 KD PROTEIN ZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDERSON K.;
Submitted (JUL-1995) to the EMBL,
-i- SIMILARITY: WEAK, TO YEAST PI
EMBL; U21321: AAB36970.1; -
WORMPEP: ZK177.6; CE02095.
PFAM; PE00400; WD40; 1
                                                                                                                                                  Q04824 PRELIMINARY;
Q04824;
01-NOV-1996 (TIEMBLIEL 0:
01-NOV-1996 (TIEMBLIEL 0:
01-JAN-1999 (TIEMBLIEL 0:
0RF6 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium. Plasmid 90 kb virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00028; cadherin; 5.
PROSTTE; PS00232; CADTERN; 5.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat Cell adhesion; Glycoprotein; 386ECA92 CRC32;
SEQUENCE 820 AA; 89864 MW; 3B6ECA92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 3:
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TISSUE-BRAIN;
                                    Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289
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Similarity 57.1%;
8; Conservative
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8; Conserv
                                                                  Proteobacteria;
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336 AA; 3
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YEAST PROTEIN CDC20.
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N ZK177.6 IN CHROMOSOME
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Last
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Pred. No. 0.49
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2DC77B26 CRC32;
                                                                  subdivision; Enterobacteriaceae;
                                                                                                                                                                                          sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                        291
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0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
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Matches 12
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01-JAN-1998
01-MAY-1999
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P. CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRRIDES N.C.,

PLEISCHMANN R.D., QUAKKENBUSH J. LEE N.H., SUTTON G.G., LOFTUS B.,

KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

PETERSON S., REICH C.I., MCMEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,

OVERBEK R., GOCAYME J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,

COTTON M.D., SPRIGGS T., ARVIACH P., KAINE B.P., SYKES S.M.,

SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                  sulphate-reducing archaeon in Nature 390:364-370(1997), EMBL; AE001080; AAB90879.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthetic genes.";
Mol. Microbiol. 8:543-558
EMBL; L08613; AAC36963.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRIEDRICH M.J., KINSEY N.E., VILA J., KADNER R.J.;
"Nucleotide sequence of a 13.9 kb segment of the 90 kb virulence
plasmid of Salmonella typhimurium: the presence of fimbrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-LT2;
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                                                                                                                                           PFAM; PF00270; DEAD; 1.
PFAM; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA REPAIR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93316852
                                                                                                                     Hypothetical SEQUENCE 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF0358
                                                                                                                                                                                                                                    ENTER J
         430
                                                                                                                                                                                                                       The complete genome sequence of the
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                       5 LLSRNTGEVRT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPMFLLSRNTGEVRT
LISRGTGEVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.2%;
| Similarity 80.0%;
| 12; Conservative
                                                        Similarity 72. 8; Conservative
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3 (TrEMBLrel. 05,
9 (TrEMBLrel. 10,
PROTEIN RAD25.
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                                                                                                                     l protein.
452 AA; 51768
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291
30683
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                                                                    52.6%;
72.7%;
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                                                                                                                      WW.
                                                        Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                           Archaeoglobus
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Last sequence update)
Last annotation update)
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Pred. No. 1.9;
O; Mismatches
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ORF6 PROTEIN.
; C4D5ADDF CRC32;
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                                                                                                                      615C80A2 CRC32;
                                                                                                                                                                                                           hyperthermophilic,
bbus fulgidus.";
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                                                                                Length 452;
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RESULT 008395

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Best Local S
Matches 7
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MEDLINE; 96181548.
PHILIPP W.J., POULET S
BALASUBRAMANIAN V., HE
                                                                                                                                                                                                                            084262;
01-NOV-1998
01-NOV-1998
01-NOV-1998
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008395;
01-JUL-1997
01-JUL-1997
01-NOV-1998
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PROSITE; PS00480; CITRATE_SYNTHASE;
PFAM; PF00285; Citrate_synt; 1.
Lyase; Tricarboxylic acid cycle.
SEQUENCE 393 AA; 42969 MW; 8850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc.
 "Genome Sequence of an Obligate Chlamydia trachomatis."; Science 0:0-0(1998).
                                                                  STEPHENS R.S.,
MITCHELL W.P.,
                                                                                                      SEQUENCE FROM N.A. STRAIN-D/UW-3/CX;
                                                                                                                                                                          Chlamydia
                                                                                                                                                                                                                                                                                                  084262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An integrated map of the c
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H37RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-H37RV;
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                                                   DAVIS R.W.;
                                                                                                                                                           Bacteria;
                                                                                                                                                                                                            HYPOTHETICAL
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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CATALYTIC ACTIVITY: C
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Chlamydiales;
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E SYNTHASES
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BLOOM B.R., JA
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                    KIMMERLY W., BONDOC M., C
KADNER K., MIGUEL T., MIL
SUBRAMANIAN S., MARTIN C.
"Sequencing of human chro
Submitted (SEP-1998) to t
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SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
STEPHENS R.S., KAI
MITCHELL W.P., OLJ
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01-JUN-1998
01-MAY-1999
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075279;
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                                                                                                            01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
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EMBL; AJ002138; CAA05206.
PFAM; PF00810; ER_lumen_r
SEQUENCE 215 AA; 25724
                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
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ALAGON A.;
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Eukaryota; Entamoebidae;
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W.P., OLINGER
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AA; 25724 MW;
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Q., KOONIN E
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SEQUENCE FROM RICKE D.O.;

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01-AUG-1998 (TrEMBLrel. C
01-MAY-1999 (TrEMBLrel. I
ASPARAGINE SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKAKIOIIO (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cr.
Eukaryota; Metazoa; Catarrhini;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA KINASE
                                                                                                                                                                                                                                                                                                                                               "Characterization of a Mutant Pancreatic eIF-2alpha Kinase, Co-localization with Somatostatin in Islet Delta Cells."; J. Biol. Chem. 274:5723-5730(1999).

EMBL; AF110146; AAD19961.1; PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

Kinase; Initiation factor.

SEQUENCE 1115 AA; 125146 MW; 5BB6FCC8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                     Elaeagnus umbellata.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheceuphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons core eudicots; Rosidae; eurosids I; Rosales; Elaeagnaceae; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Large Scale Sequence Analysis and Annotation with the Sequen Comparison Analysis (SCAN) System.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILAR EMBL; AC005609; AAC34316.1;
-- PFAM; PF00028; cadherin; 6.
PROSITE; PS00232; CADHERIN; 5.
Cell adhesion; GJycoprotein; Transmembrane; Calcium-binding; SEQUENCE 810 AA; 88391 MW; 9F4E3C7D CRC32;
TISSUE-ROOT NODULE;
KIM H.-B., AN C.-S.;
Submitted (APR-1998)
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EMBL; L40327; AAB48038.1; -
MENDEL; 9036; MEDSa;1042:1.
FFAM; PF00733; ASM_Synthase; 1.
PFAM; PF00310; GATase_2; 1.
SEQUENCE 586 AA; 66462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF061740; AF061740; AFFAM; PF00733; AFFAM; PF00310; GSEQUENCE 585 AFFAM
                                                                                     vFAS1.
Vicia faba (Broad bean).
Vicia faba (Broad bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q40328
Q40328;
01-NOV-1996
01-NOV-1996
01-MAY-1999
SEQUENCE FROM N.A.

STRAIN-KLEINE THUERINGER; TISSUE-ROOT NODULE;

KUESTER H. ALBUS U. FRREHLING M., TCHETKOVA

PUEHLER A., PERLICK A.M.;

Plant Sci. 124:89-95(1997).

-1- CAPALYZIC ACTYVITY: ATP + L-ASPARTATE + L

DIPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
                                                                                                                                                                          01-MAY-1997 (TIEMBLIEL. 03, Created)
01-MAY-1997 (TIEMBLIEL. 03, Last sequence update)
01-MAY-1999 (TIEMBLIEL. 10, Last annotation update)
ASPARAGINE SYNTHETASE (EC 6.3.5.4) (ASPARAGINE SYNTHASE
(GLUTAMINE-HYDROLYSING)) (ASPARAGINE SYNTHETASE
(GLUTAMINE-HYDROLYSING)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago sativa (Alfalfa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoid
                                                                                                                                                                                                                                                       P93618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GANTT S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-CV. SARANAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPARAGINE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                 323 TPMFLMSR 330
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                                                                                                                                                                                                                                                                                                                                              1 TPMFLLSR
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                                                                                                                                                                                                                                                                                                                                                                            Similarity 87.5%;
7; Conservative
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Similarity 87.5%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Trembirel.
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                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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; GATase_2; 1.
5 AA; 65878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC16325.1;
                                       GER; TISSUE-ROOT NODULE;
FRUEHLING M., TCHETKOVA
.M.;
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Last annotation update)
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Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB Pred. No. 45; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                   586
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                                                                                                                                                                                                                                                                                                                                                                                                       10; Length 586
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              L-GLUTAMINE -
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P
                                                   TIKHONOVITCH
                                                                                                               Papilionoideae,
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RESULT 15
024483
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Best Local Similarity
"heres 7; Conserv."
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Best Local Similarity 87.5
Watches '7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z72354; C. MENDEL; 11022; PFAM; PF00733; PFAM; PF00310; C. PFAM; PF00310; C. PFAM; PFO0310; C. PFAM; PF00310; C. P
            01-JAN-1998 (TIEMBLIEL 05, Created)
01-JAN-1998 (TIEMBLIEL 05, Last sequence update)
01-JAN-1999 (TIEMBLIEL 10, Last annotation update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
ASPARAGINE SYNTHETASE.
Medicago sativa (Alfalía).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-CENTURY; TI MEDLINE; 97188563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U77678; AAC49613.1; -. MENDEL; 8141; GLYma;1042;1. PFAM; PF00733; Asn_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetase in soybean.";

plant Mol. Biol. 33:301-311(1997).

-i- CATALYTIC ACTIVITY: ATP + L-ASPARTATE + L
DIPHOSPHATE + L-ASPARAGINE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TIEMBLIFEL 03, Created)
01-MAY-1997 (TIEMBLIFEL 03, Last sequence update)
01-MAY-1999 (TIEMBLIFEL 10, Last annotation update)
01-MAY-1999 (TIEMBLIFEL 10, Last annotation update)
ASPARAGINE SYNTHETASE 2 (EC 6.3.5.4) (ASPARAGINE SYNTHASE
(GLUTAMINE-HYDROLYSING)) (ASPARAGINE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00310; GATase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P93167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPMFLLSR 8
|||||:||
322 TPMFLMSR 329
                                                                                                                                                                                                                                                                                                                                                                                24483
                                                                                                                                                                                                                                                                                                                                            24483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGHES C.A., BEARD H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPMFLLSR 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CAA96526.1; -.
2; VICfa;1042;1.
3; Asn_synthase; 1
0; GATase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-MATURE LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66236 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
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expression of two
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Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                            586
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Search completed:
Job time: 185 sec
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE FROM N.F
MEDLINE; 97432147
SHI L., TWARY S.N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Cell 9:1339-1356(1997).
EMBL; U89923; AAB81011.1; -
PFAM; PF00733; ABR_Synthase; 1.
PFAM; PF00310; GATase_2; 1.
SEQUENCE 586 AA; 66448 MW;
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SHI L., TWARY S.N.,
SAMAC D.A., GANTT J
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                                       January 12,
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Result
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Perfect score:
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DN-cadherin - frui
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cadherin-6 - human
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cadherin-7 - chick
cadherin-6B - chic
F-cadherin - Afric
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Matches 15
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36 44 50.0 829 2 I46536											
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2 I46536  2 E70378  2 E70378  2 A38992  2 I48277  2 I48277  2 I49556  2 A53384  2 A53384  2 A27020  3 E71194  2 B71194  2 H64448  AITCAMPENTS		46.6	47.7	48.3	48.9	48.9	48.9	48.9	48.9	50.0	50.0
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## ALIGNMENTS

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F;50-615/Domain: extracellular #status predicted <EXX
F;52-157/Domain: cadherin repeat homology <CR1>
F;160-267/Domain: cadherin repeat homology <CR2>
F;270-383/Domain: cadherin repeat homology <CR2>
F;270-383/Domain: cadherin repeat homology <CR3>
F;390-495/Domain: cadherin repeat homology <CR3>
F;496-598/Domain: cadherin repeat homology <CR5>
F;616-639/Domain: transmembrane #status predicted <II
F;640-999/Domain: intracellular #status predicted <II
F;910-938/Domain: desmoglein repeat <DG1>
F;910-938/Domain: desmoglein repeat <DG2>
F;97-965/Domain: desmoglein repeat <DG2>
F;110,180,545/Binding site: carbohydrate (Asn) (cova-
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A; Cross-references: GDB:134030; OMIM:159515
A; Cross-references: GDB:134030; OMIM:159515
C; Superfamily: cadherin; cadherin repeat homology
C; Keywords: calcium binding; cell adhesion; duplication; glyc
C; Keywords: calcium binding; cell adhesion; duplication; glyc
C; 7:1-23/Domain: signal sequence #status predicted <NATS
F; 20-49/Product: desmoglein homolog #status predicted <MATS
F; 50-999/Product: desmoglein homolog #status predicted <MATS
desmoglein 1 precursor - human N;Alternate names: desmosomal glycoprotein I C;Species: Homo sapiens (man) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Accession: S16906; A39706; A61254; A61279; S16158 R;Buxton, R.S. Submitted to the EMBir-Data Library, November 1990 A;Accession: S16906 A;Accession: S16906 A;Accession: S16906 A;Molecule type: mRNA
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a A;Reference number: A41088; MUID:92069753
A;Accession: A41088
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A; Residues: 1-999 <AMA>
A; Cross-references: GB:
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R;Amagai, M.; Klaus-Kovtun,
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desmoglein 1 precursor - bovine
N;Alternate names: desmoglein BDGM
C;Species: Bos primigenius taurus (cattle)
C;Cpate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 2
C;Accession: S14603; A38872; A37785; S38721; A48173; S24412
R;Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W.
submitted to the EMBL Data Library, March 1991
A;Description: Complete sequence of the desmoglein precursor and
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A;Title: Desmosmal glycoproteins I, II and III: novel A;Reference number: A61279; MUID:92175187
A;Accession: A61279
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                                                                                   A; Reference number: S14603
A; Accession: S14603
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A;Residues: 24-1049 <
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A;Cross-references: EMBL:X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
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Residues: 1-55 <WH3>
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ross-references: GB:X56654
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2-385/Domain: cadherin repeat homology <CR3>
2-493/Domain: cadherin repeat homology <CR4>
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type: mRNA : 1-1043 <KOC>
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12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Score 74; DB
: Pred. No. 0.00
1; Mismatches
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0.0004;
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                                                         LI-cadherin human
C:Species: Homo sapiens (man)
C:Date: 15-Uul-1995 #Sequence
C:Accession: S5396
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A;Cross-references: EMBL:x57784; NID:g436061; PIDN:CAA40930.1; PID:g436062 R;Koch, P.J.; Walsh, M.J.; Schmelz, M.; Goldschmidt, M.D.; Zimbelmann, R.; Eur. J. Cell Biol. 53, 1-12, 1990 A;Title: Identification of desmoglein, a constitutive desmosomal glycoprote A;Reference number: A48173; MUID:91168965 A;Accession: A48173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:S64268; GB:S64270
R;Goodwin, L; Hill, J.E.; Raynor, K;Raszi, L; Manabe, M.; Cowin, P.
Biochem. Biophys. Res. Commun. 173, 1224-1230, 1990
A;Title: Desmoglein Shows extensive homology to the cadherin family of cell
A;Reference number: A37785; MUID:91097553
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A;Accession: A38872
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A;Residues: 44-123,'V',125-493 <GOO>
A;Cross-references: GB:M38165; NID:g162966; PIDN:AAA62709.1; PID:g552318
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submitted to the EMBL Data Library,
A; Reference number: S38721
A; Accession: S38721
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A; Residues: 1-87;968-1043 <KO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 44-1001, AQPPSAT' <KO3>
A;Cross-references: GB:X57784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 44-1043 <ZIM>
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                                                                                                                                                                                                                                                   963-1012/Region: glycine/serine-rich
110/Binding site: carbohydrate (Asn) (covalent) #status experimental
:180,496/Binding site: carbohydrate (Asn) (covalent) #status predicte
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Keywords: calcium binding; cell adhesion; duplication; 
1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                         16-875/Domain: desmoglein repeat <DG1>
76-905/Domain: desmoglein repeat <DG2>
76-905/Jomain: desmoglein repeat <CDG3>
34-962/Domain: desmoglein repeat <DG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9-574/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48/Domain: extracellular #status predicted <EXT>
                                                                                                                Local Similarity
nes 12; Conserv
                                                    1 CECNIKVKDVNDNFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Domain: cadherin repeat homology <CR1>
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cadherin repeat homology <CR3>
cadherin repeat homology <CR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intracellular #status predicted
                                                                                                                                               84.1%;
                                                                                                                                               Score 74; DB 1; Pred. No. 0.0004;
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                                                                                                                   Mismatches
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ger, A.; Kreft, B.; Fieger, to the EMBL Data Library, I

#Sequence\_revision 01-Sep-1995 #text\_change 10-Sep-1997

C: Dlouhy, B.; Berndorff, December 1994

D.; Goessner, R.;

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R;Du, Z.; Gattung, S. submitted to the EMBL Data Library, May 1997
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                    C; Date: 30 (2179)
C; Accession: A41799
R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R; Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Troyanovsky, R.; Goldschmidt, M.D.; Zimbelmann, R.; Goldschmidt, R.; Golds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
IJBODC
desmocollin 2a precursor - bovine (fragment)
N;Alternate names: epithelial type 2 desmocollin subform I
C;Species: Bos primigenius taurus (cattle)
C;Species: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 22-Jun-1999
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A;Cross-references: EMBL:X83228; NID:g854174; PID:g854175
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A; Residues: 1-832 <BO
                                                                                                                                     A;Note: sequence extracted from NCBI backbone A;Note: 264-Gln and 333-Gln were also found
                                                                                                                                                                                                           A;Cross-references: GB:M81190; NID:g163757; PIDN:AAA30782.1; A;Experimental source: muzzle
                                                                                                                                                                                                                                                                                                                                                    A; Title: Complexity and expression A; Reference number: A41799; MUID: 9: A; Accession: A41799
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A;Introns: 34/1; 114/3; 735/3; 1552/2; 1800/3; 1865/3; 1911/3; 2026/3; 2108/2; 2150/3
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A; Residues: 1-863 <KOC>
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Best Local Similarity 64.:
Matches 9; Conservative
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Best Local
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8; Conser
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Pred. No. (
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Pred. No. 1
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Б
   cadherin-related tunex suppressor precursor c;Species: Drosophila melanogaster C;Date: 30-Sep-193 #sequence_revision 30-Sep-C;Accession: A41087; B41087
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IJFFTM

30-Sep-1993

fruit fly (Drosophila melanogaster)

#text\_change 16-Feb-1997

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F;90-645/Domain: extracellular *status predicted F;92-197/Domain: cadherin repeat homology <CR1>F;200-309/Domain: cadherin repeat homology <CR3>F;312-423/Domain: cadherin repeat homology <CR3>F;426-526/Domain: cadherin repeat homology <CR4>F;527-634/Domain: cadherin repeat homology <CR4>F;527-634/Domain: cadherin repeat homology <CR4>F;527-634/Domain: cadherin repeat homology <CR5>F;527-634/Domain: cadherin repeat homology <CR4>F;527-634/Domain: cadherin repeat homology <CR4>F;527-634/Domain: cadherin repeat homology <CR4>F;527-634/Domain: cadherin repeat homology <CR5>F;527-634/Domain: cadherin repeat homology <CR5
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A; MOLECULE type: mRNA
A; Molecule type: mRNA
A; Residues: 1-809 < KOC>
A; Cross-references: GB:M81190; NID:g163757; PIDN:AAA30783.1; PID:g163759
A; Experimental source: muzzle
A; Note: sequence extracted from NCBI backbone
A; Note: sequence extracted from NCBI backbone
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N;Alternate names: epithelial type 2 desmocollin subform II
C;Species: Bos printgenius taurus (cattle)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
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;Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.;
roc. Natl. Acad. Sci. U.S.A. 89, 353-357, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90-645/Domain: extracellular #status predicted 92-197/Domain: cadherin repeat homology <CR1>200-309/Domain: cadherin repeat homology <CR2>312-423/Domain: cadherin repeat homology <CR3>426-526/Domain: cadherin repeat homology <CR4>527-634/Domain: cadherin repeat homology <CR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            646-672/Domain: transmembrane #status predicted <TMM>
673-809/Domain: intracellular #status predicted <INT>
120,346,495,579/Binding site: carbohydrate (Asn) (cov
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295
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ct: desmocollin 2a #status predicted <MAT>
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Pred. No. 3.
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MOLECULE type: DNA
MOLECULE type: DNA
Residues: 1-142;487-1278 <MA2>
;Cross-references: GB:M80537
;Cross-1229-Gly and 1233-Ser were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :Molecule type: mRNA
:Residues: 143-485;1279-5147 <MAH>
:Cross-references: GB:M80537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reference number: A41087; MUID:92069752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, ell 67, 853-868, 1991; Repressor gene in Drosophila encodes a novel member of the
                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: FlyBase:FBgn0001075
Superfamily: cadherin-related tumor suppressions; calcium binding; cell adhesion;
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                                                                               Matches
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3147/Product: cadherin-related tumor suppressor #status predicted <MAT>
1583/Domain: extracellular #status predicted <EXT>
141 EVRIKVLDVNDNSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         049/Domain: cadherin repeat homology <CR9>
1153/Domain: cadherin repeat homology <C10>
1278/Domain: cadherin repeat homology <C11>
1278/Domain: cadherin repeat homology <C12>
1384/Domain: cadherin repeat homology <C12>
1489/Domain: cadherin repeat homology <C13>
1601/Domain: cadherin repeat homology <C14>
1713/Domain: cadherin repeat homology <C15>
1923/Domain: cadherin repeat homology <C15>
1922/Domain: cadherin repeat homology <C17>
2027/Domain: cadherin repeat homology <C18>
2167/Domain: cadherin repeat homology <C19>
2278/Domain: cadherin repeat homology <C19>
2384/Domain: cadherin repeat homology <C29>
2384/Domain: cadherin repeat homology <C29>
                       2 ECNIKVKDVNDNFP 15
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Domain: cadherin repeat homology <CR3>
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by/Domain: cadherin repeat homology <CR5>
cR5>
cR6>
By/Domain: cadherin repeat homology <CR6>
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                                                                               Conservative
                                                                                                                                                                                                                                              EGF homology
                                                                                                                                                                                  transmembrane #status predicted
intracellular #status predicted
                                                                                                                                                                                                                                                                                                              cadherin
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                                                                                                                                                                                                                            EGF homology <EG4>
                                                                                                                                                                                                                                              homology <EG2>
homology <EG3>
                                                                                                  54.5%;
71.4%;
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                                                                                                  Score 48; DB 1;
Pred. No. 30;
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                                                                                 Mismatches
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                                                                                                                        Length 5147;
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RESULT

C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 20-Aug-1999
C;Accession: 145858
R;Yue, K.K.; Holton, T.L.; Clarke, J.P.; Hyam, J.L.; Hashimoto, T.; Chidgey, M.A.; Ga.
J. Cell Sci. 108, 2163-2173, 1995
A;Title: Characterisation of a desmocollin isoform (bovine DSC3) exclusively expresse A;Reference number: 145858; MUID:95403557

RESULT I45858

10

desmocollin - bovine

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A;Molecule type: mRNA
A;Rosidues: 5-516,'I',518-784 <SUZ>
A;Residues: 5-516,'I',518-784 <SUZ>
A;Cross-references: EMBL:X59796; NID:g639976; PIDN:CAA42468.1; PID:g29593
A;Cross-references: EMBL:X59796; NID:g639976; PIDN:CAA42468.1; PID:g29593
A;Campugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Ho
CCEll Biol. 118, 1511-1522, 1992
CCEll Biol. 118, 1511-1522, 1992
A;Title: A novel endothelial-specific membrane protein is a marker of cell
A;Telt. A novel endothelial-specific membrane protein is a marker of cell
A;Reference number: A43418; MUID:92394977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X79981; NID:g599833; PIDN:CAA56306.1; PID:g599834 R;Suzuki, S.; Sano, K.; Tanihara, H. Cell Regul. 2, 261-270, 1991 A;Title: Diversity of the cadherin family: evidence for eight new cadherin; A;Reference number: S24305; MUID:91283540 A;Accession: S24305
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A; Residues: 48-60,'X',62,'X',64;108-116,'X',118-123;237-238,'X',240,'X',242-252,'X',2
A; Experimental source: cultured endothelial cells
A; Note: sequence extracted from NCBI backbone (NCBIP:113040, NCBIP:113045, NCBIP:1130
C; Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are though
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 22-Jun-1999
C;Accession: S49893; S24305; A43418
R;Breviario, F; Caveda, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; L
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C; Superfamily: cadherin; cadherin repeat homology
C; Keywords: calcium binding; cell adhesion; duplication;
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-47/Domain: propeptide #status predicted <PRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;154-258/Domain: cadherin repeat homology <CR2>,261-372/Domain: cadherin repeat homology <CR3>,375-479/Domain: cadherin repeat homology <CR4>,481-587/Domain: cadherin repeat homology <CR5>,594-620/Domain: cadherin repeat homology <CR5>,594-620/Domain: transmembrane #status predicted follows for the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of th
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                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-593/Domain: extracellular #status predicted <EXT>
0-151/Domain: cadherin repeat homology <CR1>
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139 IKVHDVNDNWP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                            53/Region: serine-rich
2,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                   5 IKVKDVNDNFP 15
                                                                                                                                                                                                                   Similarity
9; Conserv
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t: cadherin 5 #status predicted <MA</pre>
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                                                                                                                                                                                                                                                               81.84;
                                                                                                                                                                                                                                                               Score 48; DB
Pred. No. 4.6;
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ZK112.7 protein - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Dece: 14-Sep-1994 #sequence_revision 12-May-1995 C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 C;Accession: $44887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A;Description: Sequence of A;Reference number: S44613 A;Accession: S44887
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                           A; Molecule type: mRNA
A; Residues: 777-1117
                                                        A;Residues: 1-1117 <ZIM>
A;Cross-references: EMBL:Z26317; NID:g416177;
A;Cross-references: EMBL:Z26317; NID:g416177;
A;Chooker P.J.; Goldschmidt, M.D.; Walsh, M.J.;
Eur. J. Cell Biol. 55, 200-208, 1991
A;Title: Complete amino acid sequence of the 6
A;Reference number: A38872; MUID:92037656
A;Accession: B38872
                                                                                                                                                                                                 R;Zimbelmann, R.
submitted to the EMBL Data
A;Reference number: S38673
A;Accession: S38673
                                                                                                                                                                                                                                                                                                            N; Alternate names: desmoglein
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A;Introns: 831/3
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A;Status: preliminary; t
A;Molecule type: mRNA
A;Residues: 1-896 <YUE>
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A; Residues: 1-3343 <DUZ>
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Best Local Similarity by...
Conservative
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                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
Date: 20-Feb-1995 #sequence_revision
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Best Local
              Cross-references: GB:S64273
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8; Conservative
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the C. elegans cosmid ZK112.
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Pred. No.
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Pred. No. 7
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7.6;
                                                                                       epidermal
                                                                                                                      PIDN:CAA81226.1;
Zimbelmann, R.;
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Franke, W.W.
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147 IKVQDINDNAP 157
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C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; duplication;
F;51-158/Domain: cadherin repeat homology <CR1>
F;161-271/Domain: cadherin repeat homology <CR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: DSG2
A; Cross-references: GDB: 1
A; Cross-references: GDB: 1
A; Map position: 18q12.1-
C; Superfamily: cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamil
C; Keywords:
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A; Residues: 1-793 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Diversity of the cadherin family: A; Reference number: S24305; MUID: 91283540 A; Accession: D38992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 13-Sep-1996 #sequence_revision
                                                                              A;Cross-references: EMBL:U59325; NID:g1389852; PIDN:AAB02933.1; C;Superfamily: cadherin; cadherin repeat homology
                                                                                                             A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-790 <SHI>
                                                                                                                                                                                        R;Shibata, T.; Shimoyama, Y.;
submitted to the EMBL Data Lil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:5822911
C;Superfamily: cadherin; cadher
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                                                                                                                                                          A; Reference number: A; Accession: G02678
                                                                                                                                                                                                                                                                    cadherin-14 -
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Best Local Similarity
Graphes 9; Consert
                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Accession: D38992
;Suzuki, S.; Sano,
                                                                                                                                                                                                                       Accession: G02678
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                                                                                                                                                                                                                                                                                                                                             148 IKVQDINDNAP
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Similarity 72.7%;
8; Conservative
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8; Conserv
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                   Score 46; I
Pred. No. 9.
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IKVKDVNDNFP

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Page 6
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TRESULT 15
TO9055

Protoccadherin 68 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999
C:Accession: T09055
R:Jin, P.; Xu, H.; Israel, D.
submitted tq the EMBL Data Library, October 1997
A:Reference number: 216540
A:Reference number: 216540
A:Reference number: 216540
A:Residues: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-889 <JIN>
A:Residues: 1-889 <JIN>
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score greater than or equal to the score of the result being printed
and is derived by analysis of the total score distribution.
  that pass the threshold
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88
1 CECNIKVKDVNDNF
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DSC2_HUMAN
IF2_AQUAE
CADI_MOUSE
CADE_HUMAN
CADE_MOUSE
CADE_RAT
YNN3_CAEEL
CADB_MOUSE
CADB_MOUSE
YNRQ_YEAST
CADB_CHICK
CADI_SCHPO
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CADI_SCHPO
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YOG7_CAEEL
CAD8_HUMAN
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CADE_HUMAN
DSG2_HUMAN
CADC_HUMAN
CADC_HUMAN
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DSG1_BOVIN
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DSC2_MOUSE
CAD5_HUMAN
CAD5_MOUSE
FAT_DROME
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15.282 Million cell updates
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caenorhabdi
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susculu
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caenorhabdi
homo sapien
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gallus gall
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DSG3_HUMAN STANDARD;
ID DSG3_HUMAN STANDARD;
AC P32926;
DT 01-0CT-1993 (Rel. 27, Cr
DT 01-0CT-1993 (Rel. 27, La
DT 01-NOV-1997 (Rel. 35, La
DE DESMOGLEIN 3 PRECURSOR (
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  TRANSMEM
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"Autoantibodies against a novel epithelial cadherin
vulgaris, a disease of cell adhesion.";

Cell 67:869-877(1991).

-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME (
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS (
FILAMENIS MEDIATING CELL-CELL ADHESION.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL,
                                                                                                                         PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  EMBL; M76482; AAA60230.1; -. PIR; A41088; IJHUG3. HSSP; P09803; 1EDH. MIM; 169615; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                      MIM; 169615; -.
PFAM; PF00028; cadherin;
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                                                                                                                                                                               Calcium-binding;
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(POTENTIAL).

(POTENTIAL).

DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3.

SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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esion; Signal; Trans
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27, Last sequence update)
35, Last annotation update)
URSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA)
     Transmembrane;
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CYTOPLASMIC (POTENT
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CADHERIN 2
CADHERIN 3
CADHERIN 4
DESNOGLEIN REPEAT 1
DESNOGLEIN REPEAT 1
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OBP_HSV6Z
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PL08_PLETR
PL11_PLETR
PL12_PLETR
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                                                                                                                      POTENTIAL.
DESMOGLEIN 3.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                             Cytoskeleton;
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                                                                                                (POTENTIAL).
                  22
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AND INTERMEDIATE
                                                                                                                                                                                             Glycoprotein;
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P36983
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Result No.

Database

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Best Local Similarity 100
Matches 15; Conservative
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                      adhesion molecules.";
Biochem. Biophys, Res. Commun. 173:1224-1230(1990).
Biochem. Biophys, Res. Commun. 173:1224-1230(1990).
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND FILAMENTS MEDIATING CELL-CELL ADHESION.
FILAMENTS MEDIATING CELL-CELL ADHESION.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGGE AND -!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOVIN
2
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. The statement is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                           KOCH P.J. WALSH M.J., SCHMELZ M.
ZIMBELMANN R., FRANKE W.W.;
"Identification of desmoglein, a
glycoprotein, as a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
Submitted (MAR-1991) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, C
01-OCT-1993 (Rel. 27, I
01-NOV-1997 (Rel. 35, I
DESMOGLEIN 1 PRECURSOR
                                                                                                                                                                                                                                   "Desmoglein shows extensive homolo
                                                                                                                                                                                                                                                                                                       "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene. Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSG1_BOVIN
Q03763;
                                                                                                                                                                                                                                                                             SEQUENCE OF 44-493 FROM
                                                                                                                                                                                                                                                                                                                                                KOCH P.J., G
FRANKE W.W.;
                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS,
                                                                                                                                                                                                                                                                                                                                                                                                                   molecules.";
Eur. J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91168965
                                                                                             - !- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
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                                                                                                             POTENTIAL).
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999
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                                                                                                                                                                                                                                                                                                                                                             GOLDSCHMIDT M.D., WALSH M.J.,
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27, Last sequence update)
35, Last annotation update)
URSOR (DESMOSOMAL GLYCOPROTEIN I)
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1; 4891F6AE CRC32;
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Pred. No. 8.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              constitutive desmosomal cadherin family of cell adhesion
                                                                                                                                                                                                                                    RASZI L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOLDSCHMIDT M.D
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Best Local S
Matches :12
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002413;

01-OCT-1993 (Rel. 27, Created)

01-OCT-1993 (Rel. 27, Last seque)

01-NOV-1997 (Rel. 35, Last annot DESMOGLEIN 1 PRECURSOR (DESMOSO)
                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-KERATINOCYTES;
MEDLINE; 91271279.
WHEELER G.N. PARKER A
                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
PIOC. Natl. Acad. Sci. U.S.A. 88:4796-4800(1991).

-I FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNI-
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND
FILAMENTS MEDIATING CELL-CELL ADHESION.

-I SUBCELLULAR-TOCATION: TYPE I MEMBRANE PROTEIN.

-I- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND E.

-I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE:

(POTENTIAL).
                                                                                    "Desmosomal glycoprotein junctions, is related to molecules.";
                                                                                                      BUXTON R.S., MAGEE A.I.; THOMAS C.L., "Desmosomal gluccome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X58466; CAA41380.1;
EMBL; X57784; CAA40930.1;
EMBL; M58165; AAA62709.1;
PIR; S14603; IJBOG1.
                                                                                                                                                                                      Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.
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12; Conservative
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Last annotation update)
R (DESMOSOMAL GLYCOPROTEIN 1)
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                                                                                              DGI, a component of intercellular desmosome the cadherin family of cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
I -> V (IN REF. 4).
MW; 13898584 CRC32;
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DESMOGLEIN REPEAT
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DESMOGLEIN REPEAT
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Pred. No. 0.00
1; Mismatches
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CADHERIN 2
CADHERIN 3
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0.00016;
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HSSP; P09803; MIM; 125670; -

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EMBL; X56654; CAA39976.1; PIR; S16906; IJHUG1.
                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                             SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
MEDLINE; 92108053.
 Complexity and expression patterns of the desmosomal cadherins.";
Proc. Nati. Acad. Sci. U.S.A. 89:353-357(1992)
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED
IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
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                                                                                                                                                                                                                                                                                                                                                      CECNIKILDVNDNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00028; cadherin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                         12; Conserv
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                                                                   GOLDSCHMIDT M.D.,
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(Rel.
2A/2B
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28, Last sequence update)

36, Last annotation update)

PRECURSOR (EPITHELIAL TYPE 2 DESMOCOLLIN)
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80.0%;
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                                                                                                                                               ta; Craniata;
Ruminantia;
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Pred. No. 0.00
1; Mismatches
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MW; FDD79961 CRC32;
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CADHERIN
                                                                   ZIMBELMANN
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POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                               ; Vertebrata; Mammalia; Pecora; Bovoidea; Bovi
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ong as its content is in no
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0.00016;
                                                                   TROYANOVSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1049;
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Matches 8
                                                         DSC2_MOUSE
P5592; 064734;
01-0CT-1996 (Rel. 34
01-0CT-1996 (Rel. 34
f 15-UUL-1999 (Rel. 37
f 15-UUL-1999 (Rel. 37
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Eutheria; [1]
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VARIANT
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SEQUENCE
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DOMAIN
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EMBL; M81190; AAA30783.1; -.
PIR; A41799; IJBODC.
PIR; B41799; IJBODD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
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         Mus musculus (Moose).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>:</u>
                                                                                                                                                  MOUSE
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PFAM; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative
                                                                                                                                                                                                     295 CIINIEDVNDNLP
                                                                                                                                                                                                                                3 CNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDER POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOF SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: FORMS 2A (SHOWN HERE) AND 2B ARE ALTERNATIVE SPLICING OF THE SAME GENE.

TISSUE SPECIFICITY: ESOPHAGUS AND RUMEN. WEAKLY IN EPIDESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: CALCIUM MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adhesion;
                                                      OR DSC3
                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00028; cadherin; 5.
PS00232; CADHERIN;
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                    STANDARD;
                                                               34, Created)
34, Last sequence update)
38, Last annotation update)
PRECURSOR (EPITHELIAL TYPE
                                                                                                                                                                                                     307
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A JENKINS N.A., GILBERT D.J., COPELAND N.G.;
AN JENKINS N.A., GILBERT D.J., COPELAND N.G.;
AN JENKINS N.A., GILBERT D.J., COPELAND N.G.;
AN JENKINS N.A., GILBERT D.J., COPELAND N.G.;
AN JENKINS N.A., GILBERT D.J., COPELAND N.G.;
AND INTERMOCOLLIN D.J., COED N.G., COPELAND N.G., COED N.G., COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INVERTAGORIA PROTEINS AND INTERMEDIATE FILAMENTS
CONDITIONS OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
CONDITIONING (STRATIFICATION) MAY CONTRIBUTE TO EPIDERMAL CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, sequence analysis and expression pattern of mous desmocollin 2 (DSC2), a cadherin-like adhesion molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GARROD D.R.;
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STRAIN-C57BL/6; TISSUE-EMBRYO;
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LORIMER J.E., HALL L.S.,
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; PF00028; ca
ECNIKVKDVNDNFP
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8; Conserv
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esion; Glycoprotein; Transmembrane; Repeat; Signal; ive splicing; Cytoskeleton; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
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Pred. No.
3; Mismatc
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CADHERIN-LIKE REP
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RT J. Cell Biol. 118:1511-1522(1992).

CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

CC -!- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

CC THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC

CC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE

CC SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A

CC IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE

CC COHESTON AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS. IT

CC ASSOCIATES WITH ALPHA-CATEVIN FORMING A LINK TO THE CYTOSKELETON.

CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. FOUND AT CELL-CELL

CC BOUNDARIES AND PROBABLY AT CELL-MATRIX BOUNDARIES.

CC -!- TISSUE SPECIFICITY: ENDOTHELIAL TISSUES AND BRAIN.

CC --- SIMILARITY BELONGS TO THE CADHERIN FAMILY.

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EMBL; X79981; CAR56306.1; -.
EMBL; U84722; AAB41796.1; -.
EMBL; X59796; CAA42468.1; -.
PIR; S24305; IJHUC5.
                                                                                   This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or.send.an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUZUKI S., SANO K., TANIHAI "Diversity of the cadherin in nervous tissue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Metazoa; Chordata; Craniata; Ver
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation (VE-CADHERIN) (CADHERIN-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAMPUGNANI M.G., RESNATI M., RAITERI M., PIGOTT R., PISACAN HOUEN G., RUCO L.P., DEJANA E.;
"A novel endothelial-specific membrane protein is a marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALI J., MULLER W.;
Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BREVIARIO F., CAVEDA L., CORADA M., MARTIN-PADURA I., NAVGOLAY J., INTRONA M., GULINO D., LAMPUGNANI M.G., DEJANA "Functional properties of human vascular endothelial cadi (784/cadherin-5), an endothelium-specific cadherin."; Agterioscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-ENDOTHELIAL CELLS; MEDLINE; 95353875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92394977
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BREIER G., BREVIARIO F., CAVEDA L., BERTHIER R., SCHNUEKCH H.,

GOTSCH U., VESTWEBER D., RISAU W., DEJANA E.;

MOLECULAR CIONING and expression of mutine vascular endothelial-
cadherin in early stage development of cardiovascular system.";

Blood 87.530-641(1996).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A MOMOPHILIC
MANNER IN CONNECTING CELLS, CADHERINS MAY THUS CONTRIBUTE TO THE

SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A

IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE

SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A

IMPORTANT ROLE IN ENDOTHELIAL CELL BIOLOGY THROUGH CONTROL OF THE

SORTING OF THE INTERCELLULAR JUNCTIONS. NERVOUS
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DOMAIN
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DOMAIN
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P55284;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN)
                                                                                                                                                                                                                                                                                                                                 MOUSE
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outStation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-BRAIN CAPILLARY;
MEDLINE; 96141083.
                                                                                                                                                                                                                                  Mus musculus (Mouse).
Mus musculus (Mouse).
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                                -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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PFAM; PF01049; Cadherin_C_term; 1.
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MIM; 601120;
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     CRC32;
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Query Match Best Local S Matches 7 243 Ŋ IKVKDVNDNFP IRLEDINDNFP 7; Conservative 15 253 54.5%; Score 48; DB Pred. No. 2.1; 4; Mismatches 멂 ۲. 0 Length 783; Indels 0, Gaps

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FAT\_DROME œ STANDARD; 5147 A

\_DROME P33450; 01-FEB-1994 01-FEB-1996 15-JUL-1998 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota; 01-FEB-1994 (Rel. 28, Created)
01-FEB-1996 (Rel. 33, Last senotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR ( (FAT PROTEIN).

EQUENCE FROM N.A. IEDLINE; 92069752.

MEDLINE; 92069/32.
MAHONEY P.A., WEBER [
GOODMAN C.S.;
GOODMAN C.S.; α: ONOFRECHUK P., BIESSMANN H., BRYANT P.J.,

member

"The fat tumor suppressor gene in Drosophila encodes a novel membe of the cadherin gene superfamily.";

Cell 67:853-868(1991),

Cell 67:853-868(1991),

-I- FUNCTION: COULD FUNCTION AS A CELL-ADHESION PROTEIN.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- DISEASE: RECESSIVE LETHAL MUTATIONS IN FAT CAUSE HYPERPLASTIC,

TUMOR-LIKE OVERGROWTH OF LARVAL IMAGINAL DISCS, DEFECTS IN

DIFFERENTIATION AND MORPHOGENESIS, AND DEAT DURING THE PUPAL

-!- MISCELLANEOUS; SIMILARITY; CONTAINS 37 CANIAN.
-!- SIMILARITY; BELCONGS TO THE CADHERIN FAMILY.
-!- SIMILARITY; CONTAINS 5 EGG-LIKE DOWAIN.
-!- SIMILARITY; CONTAINS 2 LAMININ G-LIKE DOWAI

CADHERINS-TYPE REPEATS

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EMBL: W80537: AAA28530.1: -.

PIR: A41087: IJFFTM.

HSSP: PB00740: IIXA.

FLYBASE: FB900010775: ft.

FFAM: PF00028: EGF: 4.

PFAM: PF00028: Cadherin: 34.

PFAM: PF00028: Iaminin_G: 2.

PFOSITE: PS00023: CADHERIN: 22.

PROSITE: PS00186: EGF_1: 4.

PROSITE: PS00186: EGF_1: 4.

Coll adhesion: Signal: Transmembrane: Cy
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15-JUL-1998 (Rel. 36, Last annotation update)
VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5).
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                                                                  Eutheria; Cetartiodactyla;
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PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin_C_term; 1.
PROSITE; PS00232; CADHERIN; 3.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
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28061; Q28176;
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Pred. No. 3.1;
2; Mismatches
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CADHERIN 1.
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VASCULAR ENDOTHELIAL-CADHERIN
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                     968
                                                                                    update)
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                                                                                                                                                                                                                                                                         Length 782;
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Query Match Best Local S Matches 9

9; Conservative

53.48;

Score 47; DB Pred. No. 3.5; 0; Mismatches

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Length 896

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Gaps

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SEQUENCE FROM N.A.

MEDLINE; 95403557.

YUE K.K.W., HOLTON J.L., CLARKE J.P., CHIDGEY M.A.J., GARROD D.R.;

"Characterisation of a desmocollin in the compressed in lower layers of stratification of the complex of tratification of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of t
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reflecting epithelial cell proliferation and differentiation.";

J. Cell Biol. 126:507-518(1994).

I. FINCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS. INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.

I. SUBCELLULAR LOCATION: TYPE I MEMBARNE PROTEIN.

I. ALTERNATIVE PRODUCTS: FORMS 3A AND 3B ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

I. TISSUE SPECIFICITY: STRATIFIED EPITHELIA ONLY (EPIDERMIS, TONGUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinform
the European Bioinformatics Institute. Institute of the European Bioinformatics Institutions as long modified and this statement is not remove entities requires a license agreement (State of the European Control of the European Control of the European Control of the European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control of European Control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell adhesion;
                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The bovine desmocollin family:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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DOMAIN: CALCIUM MAY
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; L33774; AAC41626.1;
; X75783; CAA53427.1;
; P09803; ISUH.
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94308280.
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989
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licing; Cytoskel
K.K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adherin; 5.
;; CADHERIN; 3.
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        MW;
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                                                                                                                                                                                                                                                                                                                CYTOPLASMIC CADHERIN 1. CADHERIN 2.
                                                         CADHERIN 5
KLHLCNOD -:
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POTENTIAL.
                                                                                                                                                                                                                                                         CADHERIN
CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Repeat; eleton; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
        I -> EF (IN REF. E5668408 CRC32;
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FORM 3B).
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01-FEB-1994 (Rel. 2)
01-FEB-1994 (Rel. 2)
15-JUL-1999 (Rel. 3)
HYPOTHETICAL 375.7
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P34616;
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                                                                                                                                                                                                                                 WORMPEP; ZK112./; LUCCEPTAM; PP00028; cadherin; 11.

PROSITE; PS00232; CADHERIN; 8.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

FROSITE; PS01186; Cell adhesion; Signal; Transmembrane;

Hypothetical protein; Cell adhesion; Signal; Repeat.

Hypothetical protein; Calcium-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., REKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
           CARBOHYD
                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                        TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATUTE 368:32-38(1994).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL)
-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. STRONG, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans.
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MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                               CHAIN
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PIR; S44887; S
                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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149
149
250
288
369
467
612
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941
941
1042
1335
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28,
38,
7 KD
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3250
3343
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288
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367
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Rhabditidae; Peloderinae; Caenorhabditi
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IN CHROMOSOME III PRECURSOR
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SEQUENCE OF 288-793 FROM N.A.
TISSUE-FETAL BRAIN;
MEDLINE; 91283640.
SUZUKI S., SANO.K., TANIHARA H.;
"Diversity of the cadherin family: ev
in nervous tissue.";
Cell Regul. 2:861-270(1991).
-!- FUNCTION: CADHERINS ARE CALCIUM!

evidence

for eight new cadherins

CALCIUM

DEPENDENT CELL ADHESION PROTEINS

MEDLINE: 95073006.

MEDLINE: 95073006.

TANIHARA H., SANO K., HEIMARK R.L., Cloning of five human cadherins cleatherin extracellular domain and g structurally different types of cat Cell Adhes. Commun. 2:15-26(1994).

R.L., ST JOHN T., SUZUKI S.; is clarifies characteristic features of nd provides further evidence for two cadherin.";

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Best Local S
Matches 8
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CADB_HUMAN
P55286;
01-OCT-1996
01-OCT-1998
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                STRAIN-SWISS WEBSTER / MEDLINE; 97174321.
KOREMATSU K., REDIES C.
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                                           SEQUENCE FROM N
                                                           Eutheria;
                                                                    Eukaryota;
                                                                             Mus musculus
(OREMATSU K., REDIES C.;
'Restricted expression of cadherin-8 in segmental
subdivisions of the embryonic mouse brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORTING OF HETEROGENEOUS CELL TYPES, SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: MAINLY EXPRESSED IN BRAIN. FOUND IN CERTAINTSUE SPECIFICITY: MAINLY EXPRESSED IN BRAIN.
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Homo sapiens (Human) Eukaryota; Metazoa;

Primates;

Chordata; C Catarrhini;

Craniata; Vertebrata; Mammalia; i; Hominidae; Homo.

SHIBATA T., SHIMOYAMA Y., GOTOH M., HI
"Identification of human cacherin 14,
II cacherin, by protein interaction of
J. Biol. Chem. 272:5236-5240(1997).

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FUNCTION: CADHERINS

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TISSUE-BRAIN; MEDLINE; 97184182. SHIBATA T., SHIMOY

Eutheria; Pri [1]. SEQUENCE FROM

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FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CEITHEY PREFERENTIALLY INTERACT WITH THEMSELVES
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HSSP; P15116; 1NCI.
PFAM; PF00028; cadherin; 5.
PFAM; PF01049; cadherin_C_term; 1.
PROSITE; PS00232; CADHERIN; 3.
Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane;
                                                                                                                                                                                                              TISSUE-COLON CARCINOMA;
MEDLINE; 94192736.
SCHARFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human desmoglein,
"Expression catalogue of the desmoglein subfamily of
cadherins";
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                                                                 SEQUENCE OF 777-1117 FROM N.A. MEDLINE; 92037656.
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COCH P.J., GOLDSCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE W.W., Complete amino acid sequence of the epidermal desmoglein precursor
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
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075284 homo sapien
054800 rattus norv
054801 rattus norv
054801 rattus norv
050622 homo sapien
015202 homo sapien
                                                                                                           055134 mus musculu
013737 schizosacch
075279 homo sapien
075288 homo sapien
095206 homo sapien
062328 caenorhabdi
075287 homo sapien
035542 mus musculu
088689 mus musculu
077704 canis famil
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090425 brachydanio
015336 homo sapien
012864 homo sapien
001912 caenorhabdi
024298 drosophila
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                                                           Q90425 PRELIMINARY;
Q90425;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAY-1999 (TrEMBLrel. 1
VENTRAL NEURAL CADHERIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     035902 PRELIMINARY;
035902;
01-JAN-1998 (TrEMBLrel. 0)
01-JAN-1998 (TREMBLrel. 0)
01-MAY-1999 (TREMBLrel. 1)
DESMOGLEIN 3 (FRAGMENT).
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Brachydanio rerto (Zebrafish) (Zebra danio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                       251 CECSIKIKDVNDNFP
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13; Conserv
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01, Last sequence update)
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Q634292
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Q13129
Q93300
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Q67056
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075286
075309
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3.2e-05;
hes 0;
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0752861
0753091
024292
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055122
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067056 a
008174 h
0081753 h
0015053 h
075277 h
075280 h
075282 h
075282 h
075282 h
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Best Local Similarity 91./
Matches 11; Conservative
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Q15336;
                                                                                                                                                                                           Q12864 PRELIMINARY; PRT; 832 AA. Q12864; Q1.1864; Q1. Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1999 (TrEMBLrel. 10, Last annotation update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) INTESTINAL PEPTIDE-ASSOCIATED TRANSPORTER HPT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOETTINGER A., KREFT B., FIEGER C., DLOUHY B., BERNDORFF D., GOESSNER R., TAUBER R.;
SUBMITTED (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; X83228; CAA58231.1; --
PFAM; PF00028; Cadherin; 7.
PROSITE; PS00232; CADHERIN; 3.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeating B32 AA; 92207 MW; 65C9ZD4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLIEGL 01, 01-NOV-1996 (TREMBLIEGL 01, 01-MAY-1999 (TREMBLIEGL 10,
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PFAM; PF00028; cadherin; 3.

PFAM; PF01049; Cadherin_C_term; 1.

PROSITE; PS00232; CADHERIN; 1.

ZFIN; ZDB-GENE-980526-170; vnc.

Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat.

NON_TER

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
FRANKLIN J.L., SARGENT T.D.;
Dev. Dyn. 206:0-0(0).
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
MEDLINE; 94204643
DANTZIG A.H., HOS
                                                      TISSUE-COLON
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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9; Conservative
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  HOSKINS
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Pred. No. 1.6;
3; Mismatches
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Pred, No. 0.16;
); Mismatches 1
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  L.B.,
  BRIGHT
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  SHEPARD
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                                                                                                                                                           Mammalia;
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Best Local S
Matches 9
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STRAIN-BRISTOL N2;
DU Z., GATTUNG S.;
Submitted (MAY-1997)
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001912;
01-JUL-1997
01-JUL-1997
01-MAY-1999
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSO
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPEA, SUUNDERS D., SHOWNKEJ
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U07969; AAA19021.1; --
PFAM; PF00028; cadherin; 7.
PROSITE; PS00232; CADHERIN; 3.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding;
SEQUENCE 832 AA; 92147 MW; B5193483 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JENKINS I.L., DUCKWORTH D.C., SPO

ROSTECK P.R., SKATRUD P.L.;

"Association of intestinal peptid

to the cadherin superfamily.";

Science 264:430-433(1994).

-!- SUBCELLULAR LOCATION: TYPE I
                                                                                WATERSTON R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY S:
EMBL; AF003388; AAB54266.1; -
PFAM: PF00001; 7tm_1; 1.
PFAM: PF00028; cadherin; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 94150718.
PROSITE; PS00232; CADHERIN; 8.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; SEQUENCE 2163 AA; 238609 MW; 6C85C652 CRC32;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditina;
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Similarity 64.3%;
9; Conservative
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7 (TrEMBLrel. 04, Last sequ
9 (TrEMBLrel. 10, Last anno
TO MULTIPLE CADHERIN-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Last annotation update)
ERIN-TYPE REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein related
                                                                                                                                                                     SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOHNSTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHOWNKEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COULSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                               Repeat
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Query Match 58.0%; Best Local Similarity 53.3%; Matches 8; Conservative

Score 51; DB Pred. No. 5.9; 3; Mismatches

5.9;

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Length 2163

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00232; CADHERIN; 5.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
FLYBASE; FBgn0003391; Shg.
PFAM; PF00028; Cadharia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q24298;
Q24298;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAY-1999
 CARBOHYD
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"A Drosophila homolog of cadherin associated with armadillo and essential for embryonic cell-cell adhesion.";

Dev. Biol. 165:716-726(1994).

-i. FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTE THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORFING OF HETEROGENEOUS CELL TYPES.

N. CADHERIN MAY BE INVOLVED IN NEURONAL RECOGNITION MECHANISM.

-i. SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TIN EDITORITY: STAGE 10 EMBRYOS EXHIBIT INTENSE EXPRESSION PROTEIN.
                                                                                                                                                                    DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                     Signal
Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NAY-1999 (TrEMBLrel. 10, Last annotation
DE-CADHERIN PRECURSOR (SHOTGUN) (SHG).
SHG OR GP150 OR DE-CADHERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H.
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NERVOUS SYSTEM SHOW STRONG EXPRESSION.
SIMILARITY: BELONGS TO THE CAPHERIN FAMILY.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
L; D28749; BAA05942.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAGE 14 EMBRYOS SHOW EXPRESSION IN THE HINI (AT THE APICAL POLES OF CELL-CELL BOUNDARIES JUNCTIONS OF TRACHEAL CELLS AND IN THE DORES IN STAGE 16 EMBRYOS THE GLIAL MIDLINE CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN EPITHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00028; cadherin; 7.
PF01049; Cadherin_C_term;
PF00054; laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95046887.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
 1507
13207
1349
1349
11507
1123
522
522
523
623
733
837
466
813
766
949
949
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1073
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                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
EGF-LIKE.
CADHERIN 1 (CR1).
CADHERIN 2 (CR2).
CADHERIN 3 (CR3).
CADHERIN 4 (CR4).
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
DE-CADHERIN PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                      CADHERIN
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND TISSUE SPECIFICITY
                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN THE HINDGUT
                                                                                                                                                                      (CR1).
(CR2).
(CR3).
(CR4).
(CR5).
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on update)
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a; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DORSAL
                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ċ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTENSE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE CENTRAL
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RESULT
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Best Local S
Matches 10
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Best Local S
Matches 7
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                      013737;
  TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                       EMBL;
                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                     01-JUN-1998 (TIEMBLIE1. 06, Created 01-MAY-1999 (TIEMBLIE1. 10, Last se 01-MAY-1999 (TIEMBLIE1. 10, Last an HYPOTHETICAL 24.9 KD PROTEIN C16E8 CRACIERS 02
                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00028; cadherin; 5.
PROSITE; PS00232; CADHERIN; 5.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat.
SEQUENCE 1180 AA; 128672'MW; 48C0883F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                    Hypothetical
TRANSMEM
                                                        -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: TO YEAST YEAST YEAST, Z98529; CAB11031.1;
                                                                                            Submitted (AUG-1997)
                                                                                                     STRAIN-972;
OLIVER K.,
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                 SPAC16E8.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELO P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
NISSUE-BRAIN CAPILLARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTOCADHERIN-
                                                                                                                                                                                                                                                                                                                       336 CKVLIKVLDVNDNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 CTFNVTIEDINDNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HBL; Y08715; CAA69965.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                        1 CECNIKVKDVNDNFP
                                                                                                                                                                                                                                                                                                                                                                    56.8%;
l Similarity 66.7%;
l0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 46.7; Conservative
                                                                                                       HARRIS
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1290
1507
protein;
65
8:
105
135
135
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1290
169854 >
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  47
125
155
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Sciurognathi; Muridae; Murinae;
 1; Transmembrane.
47 POTENTIAL.
85 POTENTIAL.
125 POTENTIAL.
155 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                              15
                                                                                            to the
                                                                               BARRELL B.G., RAJANDREAM M.A., WO
co the EMBL/GenBank/DDBJ databases
CON: INTEGRAL MEMBRANE PROTEIN (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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                                                                     ACTOTOM
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TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
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POTENTIAL.
4 MW; 911CC772
                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB Pred. No. 4.7; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                  PRT;
                                                                     AND
                                                                                                                                                                                                        sequence update)
annotation update)
E8.02 IN CHROMOSOME
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                                                                     SOME,
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                                                                       or
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                                                                    ROTEIN (POTENTIAL).
N.CRASSA ATP-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1507;
                                                                                                                                                                                                                                                                                                                                                                                         Length 1180;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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Mus.
                                                                                                     WOOD V.;
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SEQUENCE FROM N.A.

KIMMERLY W., BONDOC M., CHENG J., C
KADNER K., MIGUEL T., MILLER C., PI
SUBRAMANIAN S., MARTIN C.H.;
"Sequencing of human chromosome 5."
Submitted (SEP-1998) to the EMBL/Ge
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                                                                                                                           HOMO sapiens (Human).
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Ca
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MEDLINE; 99005335.
STREHL S., GLATT K., I
"Characterization of t
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PROSITE; PS00232; CADHERIN; 5.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; SEQUENCE 936 AA; 98879 MW; 3A6F1EC8 CRC32;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE; 94150718.
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTWING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,
PARSONS J., PERCY C., MCMURRAY R., MORTIMORE B., O'CALLACHAN M.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                            "Large Scale Sequence Analysis and Annotation Comparison Analysis (SCAN) System."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEMBL; AC005609; AAC34324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIMMERLY W., BONDOC M., CHENG J., CO
KADNER K., MIGUEL T., MILLER C., PIT
SUBRAMANIAN S., MARTIN C.H.;
"Sequencing of human chromosome 5.";
Submitted (SEP-1998) to the EMBL/Gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Ci
Eutheria; Primates; Catarrhini;
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01-NOV-1998 (TremBlrel.
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SEQUENCE 824
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.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                                                                                                                                                                                              ACOO5609; AACUTULE
PE00028; cadherin; 5.
PEF000232; CADHERIN; 5.
PATHON GIYCOPTOTEIN; Transmembrane; Calcium-binding;
PATHON GIYCOPTOTEIN; TSANSMEMBRANE; CALCIUM-binding;
PATHON GIYCOPTOTEIN; TSANSMEMBRANE; CALCIUM-binding;
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Pred. No. 5.3;
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ROJESKI
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MATSUYOSHI N., TODA K.
TAKEICHI M., IMAMURA S
"IN vivo evidence of t
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01-NOV-1998
01-XAY-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular integrity.";

Proc. Assoc. Am. Physicians 109:362-371(1997).

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILAR EMBL; D63942; BAA22617.1;

-EMBL; D63942; BAA22617.1;

-FRAM; PF00028; cadherin; 5.

FFAM; PF01049; Cadherin_C_term; 1.

PROSITE; P800232; CADHERIN; 3.

cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; SEQUENCE 784 AA; 87902 MW; 68D4FB78 CRC32;
                                                                                                     KOHMURA N., SENZAKI K., HAMADA S., KAI N., YASUDA R., WATANAB ISHII H., YASUDA M., MISHINA M., YAGI T.;

"Diversity revealed by a novel family of cadherins expressed neurons at a synaptic complex.";

Neuron 20:1137-1151(1998).

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILAR EMBL; D86916; BAA29045.1; -..

PERM, PF00028; cadherin; 6.

PROSITE; PS00232; CADHERIN; 5.

Cell adhesion; 61ycoppotedin; Transmembrane; Calcium-binding; SEQUENCE 947 AA; 103143 MW; AB588B2C CRC32;
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Eukaryota; Metazoa; C
Eutheria; Rodentia; S
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Eutheria; Rođentia;
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01-MAY-1999
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                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
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l to the score of the result being printed,
                                                      VGIHLY
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## ALIGNMENTS

desmoglein 3 precursor - human
N;Alternate names: pemphigus vulgaris antigen
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993

RESULT

Cell 67, 869-877,

R; Amagai, M.; Klaus-Kovtun, V.;

Stanley, J.R.

#text\_change 22-Jun-1999

C; Accession: A41088

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desmoglein 1 precursor - human ();Alternate names: desmosomal glycoprotein I C;Species: Homo sapiens (man) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Accession: S16906; A39706; A61254; A61279; S16158
R:Buxton, R.S.
submitted to the EMBL_Data Library, November 1990
A;Reference number: $16906
A;Accession: $18906
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;50-615/Domain: extracellular *status predicted <EXT>
F;52-157/Domain: cadherin repeat homology <CRL>
F;160-267/Domain: cadherin repeat homology <CRL>
F;270-383/Domain: cadherin repeat homology <CR3>
F;270-383/Domain: cadherin repeat homology <CR3>
F;390-495/Domain: cadherin repeat homology <CR3>
F;490-598/Domain: cadherin repeat homology <CR5>
F;496-598/Domain: transmembrane *status predicted <INT:
F;640-999/Domain: intracellular *status predicted <INT:
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A;Accession: A41088
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C; Superfamily: cadherin; cadherin repeat homology
C; Keywords: calcium binding; cell adhesion; dupli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-999 < AMA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: calcium binding; cell adhesion; duplication; 1-23/Domain: signal sequence *status predicted <SIG>24-49/Domain: propeptide *status predicted <PRO>50-999/Product: desmoglein homolog *status predicted <W
                                                                                                                                                                                                                                                                                                                                                                            79
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Pred. No.
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hes 0;
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desmoglein i previous desmoglein BDGM N;Alternate names: desmoglein BDGM C;Species: Bos primigenius taurus (cattle) C;Species: Bos primigenius taurus (cattle) C;Date: 30-Jun-1993 **text_change C;Date: 30-Jun-1993 **sequence_revision 30-Jun-1993 **text_change C;Accession: S14603; A38872; A37785; S38721; A48173; S24412 R;KOch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W. submitted to the EMBL Data Library, March 1991 **.nearrintion: Complete sequence of the desmoglein precursor and
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A;Cross-references: EMBL:X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
R;Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Ataliotis, P.; Poynter, D.; Arnemann, Proc. Natl. Acad. Sci. U.S.A. 88, 4796-4800, 1991
A;Title: Desmosomal glycoprotein DGI, a component of intercellular desmosome junct: A;Reference number: A39706; MUID:91271279
                                          A;Description: Complete sequence
A;Reference number: $14603
A;Accession: $14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Arnemann, Blochem. Soc. Trans. 19, 1060-1064, 1991
A;Title: Desmosomal glycoproteins I, II and III: novel A;Reference number: A61279; MUID:92175187
A;Accession: A61279
                                                                                                                                                                                                                                                                                                            desmoglein 1 precursor - bovine
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C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; dupli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \;Residues:
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A;Reference number: A61254; MUID:92121251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7549-569/Domain: transmembrane #status predicted <TMM>
7572-1049/Domain: intracellular #status predicted <INT>
75840-869/Domain: desmoglein repeat <DG1>
7840-869/Domain: desmoglein repeat <DG2>
7870-899/Domain: desmoglein repeat <DG3>
7900-927/Domain: desmoglein repeat <DG3>
7928-956/Domain: desmoglein repeat <DG4>
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Best Local
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Cross references: GS.X56654
NILLES, L.A.; PARTY, D.A.D.; Powers, E.E.;
Cell Sci. 99, 809-821, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Residues: 24-1049 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-49/Domain: propeptide #status predicted <PRO>50-1049/Product: desmoglein #status predicted <MAT>50-548/Domain: extracellular #status predicted <EXT>
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10-269/Domain: cadherin repeat homology <CR2>
2-385/Domain: cadherin repeat homology <CR3>
2-493/Domain: cadherin repeat homology <CR4>
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2; Mismatches
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0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1049;
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                                                                                                                                                                                                      22-Jun-1999
                                                                                                            evidence
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A;Cross references: GB:564268; GB:S64270
R;Goodwin, L.; Hill, J.E.; Raynor, K.; Raszi, L.; Manabe, M.;
Biochem. Biophys. Res. Commun. 173, 1224-1230, 1990
A;Title: Desmoglein shows extensive homology to the cadherin file.
A;Reference number: A37785; MUID:91097553
A;Moleculo.
                                                                                                                                                         RESULT
                                               phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) - cowpea N;Alternate names: AIR synthase; AIRS; phosphoribosylaminoimidazole C;Species: Vigna ungui<del>ra</del>nta (cowpea) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-S
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A;Reference number: S38721
A;Accession: S38721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;180,496/Binding site:
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A; Residues: 44-1043 <ZIM>
A; Residues: 44-1043 <ZIM>
A; Cross-references: EMBL:X57784; NID:g436061; PIDN:CAA40930.1; PID:g436062
R; Koch, P.J.; Walsh, M.J.; Schmelz, M.; Goldschmidt, M.D.; Zimbelmann, R.;
Eur. J. Cell Biol. 53, 1-12, 1990
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A;Residues: 44-123,'V',125-493 <GOO>
A;Cross_references: GB:M58165; NID:g162966; PIDN:AAA62709.1; PID:g552318
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Best Local S
Matches 12
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;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
;180,496/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,575-1043/Domain: intracellular #status ;646-875/Domain: desmoglein repeat <DG1>,876-905/Domain: desmoglein repeat <DG2>,876-995/Domain: desmoglein repeat <DG3>,906-933/Domain: desmoglein repeat <DG3>,934-962/Domain: desmoglein repeat <DG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 44-1001, 'AQPPSAT' <KO3>
Cross-references: GB:X57784
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272-385/Domain: cadherin repeat homology <CR3>
392-491/Domain: cadherin repeat homology <CR4>
549-574/Domain: transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3/Domain: signal sequence #status predicted <SIG>
49/Domain: propeptide #status predicted <PRO>
1043/Product: desmoglein #status predicted <MAT>
548/Domain: extracallular #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                            ATOKITYRISGVGID 15
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12; Conser
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                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                86.5%;
Goggin,
                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB Pred. No. 0.00 2; Mismatches
D.EI.
                                                    16-Jul-1999 #text_change 24-Sep-1999
Atkins,
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0.0014;
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Plant Mol. Biol. 36,
A;Title: AIR syntheta
A;Reference number: Z
A;Accession: T10963
                                                                                                                                                                                         A; Map position:
C; Superfamily: c
C; Keywords: carb
F; 422-470/Domain
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R;Chasse, J.F.; Paris, D.; Paly, E.; Kamoun, P.; London, J.
submitted to the EMBL Data Library, October 1994
A;Description: Characterization of human cystathionine beta-synthase
A;Reference number: S49459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 91, 6614-6618, 1994
A;Title: A yeast system for expression of human cystathionine
A;Reference number: A55760; MUID:94294429
A;Accession: A55760
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A;Experimental source: strain Vita 3; root nodule; clone pAIRS19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: mRNA
;Residues: 1-360/A',362-364,366-418,'G',420-492,'L',494-498,'R',500-543,'V',545-552
;Cross-references: GB:L19501; NID:g388715; PIDN:AAA19874.1; PID:g388716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Human cystathionine beta-synthase cDNA: sequence, alternative splicing; Reference number: I54342; MUID:94093551; Accession: I54342
                                                                                                                                                                                                                                Superfamily: cystathionine beta-synthase; CBS Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                  Cross-references:
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Residues: 1-552 <KRU>
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AIR synthetase in
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                                           56.8%;
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Score 42; DB
Pred. No. 7.4;
4; Mismatches
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Pred. No.
                                       42;
No. 7
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TOKITYRISGYGID

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R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, submitted to the EMBL Data Library, November 1997 A;Description: Arabidopsis thaliana chromosome II BAC T517 genomi A;Reference number: Z14159 A;Accession: T01000
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A; Reference number: 217611
A; Accession: T13154
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A;Molecule type: DNA
A;Residues; 1-897 <HAN>
A;Cross-references: GB:M35107
C;Keywords: glycosidase; hydrolase
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A;Title: Expression and nucleotide sequence of the Clostridium acetobutylicum beta-ga
A;Reference number: A39405, MUID:91216979
A;Accession: A39405
                                                                                                  hypothetical protein T517.1 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999
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7; Conserv
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72.7%;
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3; Mismatches
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A; Molecule t
A; Residues:
A; Cross-refe
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R;Bornstein, P.; Devarayalu, S.; Edelhoff,
Genomics 15, 607-613, 1993
A;Title: Isolation and characterization of
A;Reference number: A46016; MUID:93224149
A;Accession: A46016
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                   thrombospondin 3 - mouse
C;Spectes: Mus musculius (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: A46016; A44124; T55398; S68788; S72433
R;Bornstein, P.; Devarayalu, S.; Edelhoff, S.; Disteche, C.M.
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A;Residues: 1-441 <ROU>
A;Cross-references: EMBL:AC003000; NID:g2642152; PID:g2642153
                                                                             A; Reference number: A44124; MOID:92291102
                                                                                                      A;Cross-references: GB:L04302; NID:g202200; PIDN:AAA40497.1; A;Note: sequence extracted from NCBI backbone (NCBIN:19415, R:Vos, H.L.; Devarayalu, S.; de Vries, Y.; Bornstein, P. J. Biol. Chem. 267, 12192-12196, 1992
A;Title: Thrombospondin 3 (Thbs3), a new member of the thromb
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A; Introns: 202/1;
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A;Title: Genomic organization of the human myocilin gene (MYOC) responsible A;Reference number: JC5830; MUID:98113364
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C:Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C:Accession: JC5830
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A; Residues: 1-956 <BOR>
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:Residues: 1-504 <KUB>
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references: GB:M86620;
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               type: DNA : 517-956 < VOS>
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54.5%;
NID: g201987; PIDN: AAA40430.1;
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Pred. No.
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Pred. No. 24;
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NCBIP: 129416;
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A: Map position: 4
C: Superfamily: Ar
C: Keywords: ATP
F: 439-653/Domain:
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A; Variety: columbia
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: D71416
C; Accession: D71416
P; Wedler, E; Bent, E; Love, K; Goodman, H; Dean, C; Bergkamp, R; P; Bevan, M; Bancroft, I.; Bent, E; Love, K; Goodman, H; Dean, C; Bergkamp, R; P; Wedler, H; Wedler, E; Wambutt, R; Weitzenegger, T; Pohl, T.M.; Terryn, N; Funk, avanagh, T; Hempel, S; Kotter, P; Entian, K, D; Rieger, M; Schaeffer, M; Funk, Nature 391, 485.488, 1998
Nature 391, 485.488, 1998
                                                                                                                                                                                                               A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N. Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t A;Reference number: A71400; MUID:98121113
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Nucleic Acids Res. 24, 3661-3669, 1996
A;Title: SP1-binding elements, within the
A;Reference number: $72433; MUID:97025352
A;Accession: $72433
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A; Residues: 1-1177 <
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A; Residues: 1-26 <COL>
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A; Residues: 1-432,'F',434-562,'D',564-719,'E',721-870,'W',872-956 <RES>
A; Residues: GB:L24434; NID:g402718; PIDN:AAA40433.1; PID:g402719
R; Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Qabar, A.N.; Lin, Z.; Wolf, F.W.; O'Shea, J. Biol. Chem. 269, 1262-1269, 1994
A:Title: Thrombospondin 3 is a developmental
                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable PDR5-like ABC transporter -
C;Species: Arabidopsis thaliana (mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Complex: homopentamer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 'X', 23-28, 'X', 30, 'X', 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complex: homopentamer, disulfide linked;
Superfamily: thrombospondin 3; EGF homology;
Keywords: calcium binding; glycoprotein; homopentamer;
310,407,644,937/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: I55398; MUID:94117438
Accession: I55398
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Best Local
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                                                                                                  Genetics:
                                                                                                                                                                                             Status: preliminary; nucleic acid sequence
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7; Conser
                                              : 4COP9-4G3845
Arabidopsis thaliana
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                                                                                                                                                   ABEV>
                                                                                                                       GB: Z97338; NID: g2244870;
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Pred. No.
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72;
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                                                                                                                       PID:e326915;
                                                                                                                                                                                               not shown; translation not shown
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439-653/Domain: ATP-binding cassette

probable

PDR5-like

ABC

transporter; ATP-binding

homology <ABC2>

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A; Cross-rete
C; Superfamil
C; Keywords:
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A;Title: 3-Hydroxy-3-methylglutaryl coenzyme A lyase (HL): clc A;Reference number: 157009; MUID:93364116
A;Accession: 157009
            hydroxymethylglutary1-CoA lyase (EC 4.1.3.4) - Arabidopsis W;Alternate names: protein F12C20.16 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_ch C;Accession: T02655
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B45470
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C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 25-Mar-1998
C:Accession: B45470
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C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C;Accession: 157009
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Matches 6
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Best Local
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6; Conserv
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9; Conser
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C.M.; Lin,
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Pred. No. 20;
5; Mismatches
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22;
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  K.A.; Crosby,
                          #text_change 22-Jun-1999
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  M.L.; Brandon,
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A; Experimental so
C; Genetics:
A; Map position: 2
A; Introns: 55/2;
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C; Superfamily: hydroxymethylglutaryl-CoA lyase
C; Keywords: carbon-carbon lyase; oxo-acid-lyase
                                                                                                               A;Gene: purM
C;Superfamily: phosphoribosylformylglycinamidine cyclo·ligase;
F;4-317/Domain: phosphoribosylformylglycinamidine cyclo·ligase
                                                                                                                                                                                                                                                                                             A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A; Reference number: A70300; MUID:98196666
A; Accession: E70367
                                                                                                                                                                                                                                                                                                                                                                                                         phosphoribosylformylglycinamidine cyclo-ligase -
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-199
C;Accession: E70367
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A; Residues: 1-433 <ROU>
A; Residues: 1-433 <ROU>
A; Cross-references: EMBL: AC005168; NID: 93426033;
A; Experimental source: cultivar Columbia
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                                                                                                                                                                                   A; Experimental source: C; Genetics:
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A; Residues: 1-331 <AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                     Nature 392, 353-358, 1998
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                                    Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                              Status:
                                                                                                                                                                                                        Cross-references: GB:AE000706; NID:g2983327; PIDN:AAC06918.1; Experimental source: strain VF5
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   5 ITYRISGYGID 15
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                                                         No.
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                                                                       Length 331;
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                                        Indels
                                                                                                                                                                                                                                                                               translation not shown
                                                                                                                             phosphoribosylformylgl homology <PFCL>
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Title: Perfect

score:

US-08-991-628-1 74

ATQKITYRISGVGID

Scoring table: Sequence

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   DSG3_HUMAN
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MYOC_HUMAN
MYOC_HUMAN
MYOC_HUMAN
MYOC_YOUSE
CBS_RAT
TSP3_MOUSE
CBS_RAT
TSP3_MOUSE
CBS_RAT
TSP3_WOUSE
CVBLOVBLY
VG12_CVBLO
VG12_CVBLO
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15.282 Million cell updates/sec
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6 phaseolus a
5 neisseria g
6 clostridium
8 arabidopsis
7 haemophilus
8 homo sapien
9 homo sapien
6 aspergillus
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9 dallus gall
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01-OCT-1993
01-NOV-1997
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DSG3_HUMAN
P32926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMAGAI M., KLAUS-KOVTUN V., STANLEY J.R.;
"Autoantibodies against a novel epithelial cadherin
vulgaris, a disease of cell adhesion.";
Cell 67:869-877(1991).
-i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JI
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AL
FILAMENTS MEDIATING CELL-CELL ADHESION.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL, E
                                                                                                                                                                                                                                                                                                         EMBL; M76482; AAA60230.1;
PIR; A41088; IJHUG3.
HSSP; P09803; 1EDH.
MIM; 169615; -
                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A MEDLINE; 92069753
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DESMOGLEIN 3 PRECURSOR (130 KD PEMPHIGUS VULGARIS ANTIGEN) (PVA).
                                                                                                                                                                                                                                      Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3.

SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARCINOMAS.

DOMAIN: CALCIUM MAY BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (Human).
ryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
eria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00028; cadherin; 4.
PS00232; CADHERIN; 3.
esion; Signal; Transmembrane;
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893
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607
POTENTIAL.

DESMOGLEIN 3.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CADHERIN 1.

CADHERIN 2.

CADHERIN 3.

CADHERIN 4.

CADHERIN 4.

DESMOGLEIN REPEAT 1.

DESMOGLEIN REPEAT 2.

POTENTIAL.
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CRU3_BRANA
DSC1_BOVIN
DSC1_HUMAN
DSC2_BOVIN
G6PI_TRYBB
                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUNCTIONS.
AND INTERMEDIATE
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P33525
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Result No.

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Best Local :
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01-OCT-1993
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOCH P.J., WALSH M.J., SCHMELZ M., GOLDSCHMIDT M.D., ZIMBELMANN R., FRANKE W.W.; "Identification of desmoglein, a constitutive desmosomal glycoprotein, as a member of the cadherin family of cell molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
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SEQUENCE
                                                                                                                                                                                                           adhesion molecules.";
Blochem. Blophys. Res. Commun. 173:1224-1230(1990).
Blochem. Blophys. Res. Commun. 173:1224-1230(1990).
i- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATING CELL-CELL ADHESION.
IFILAMENTS MEDIATING CELL-CELL ADHESION.
I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
I- TISSUE SPECIFICITY: EPIDERMIS, MUZZLE, TONGGE AND ESOPHAGUS.
I- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene."; Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHNIDT M.D.,
Submitted (MAR-1991) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, 01-OCT-1993 (Rel. 27, 101-NOV-1997 (Rel. 35, 101-NOV-1997 (Rel. 37, 101-NOV-1997 (Rel. 35, 1
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                                                                                                                                                                                                                                                                                                                                                                                                            GOODWIN L., HILL J.E., RAYNOR K., RASZI "Desmoglein shows extensive homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 44-493 FROM N.A. MEDLINE: 91097553.
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Q03763;
                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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15; Conser
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Metazoa;
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27, Last sequence update)
35, Last annotation update)
WRSOR (DESMOSOMAL GLYCOPROTEIN
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s 0;
                                                                                                                                                                                                                                                                                                                                                                                                            MANABE M., COWIN cadherin family
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3J databases.
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AND INTERMEDIATE
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AC 002413;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-OCT-1993 (Rel. 35, Last annotation update)

TO 01-NOV-1997 (Rel. 35, Last annotation update)

TO 01-NOV-1997 (Rel. 35, Last annotation update)

TO 01-NOV-1997 (Rel. 35, Last annotation update)

TO 01-NOV-1997 (Rel. 35, Last annotation update)

TO 01-NOV-1997 (Rel. 35, Last annotation update)
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Best Local S
Matches 12
                                                                                  MEDLINE; 91271279.
WHEELER G.N., PARKER A.E., PI
ARNEMANN J., RUTMAN A.J., PI
BUXTON R.S., MAGEE A.I.;
"Desmosomal glycoprotein DGI
junctions, is related to the
molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
         Proc. Natl. Acad. Sci. U.S.A. 88:4796-4800(1991).
-!- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEL
FILAMENTS MEDIATING CELL-CELL ADHESION.
-!- SUBCELLULAR BOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR BOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND ESOPHAGUS
-!- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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EMBL; X57784; CAA40930.1;
EMBL; M58165; AAA62709.1;
PIR; S14603; IJBOG1.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3 MW; 13898584 CRC32;
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DESMOGLEIN REPEAT 5
                                                                                               , a component of intercellular desmosome cadherin family of cell adhesion
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WATT F.M., RE
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PIR; S16906;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
PHOSPHORIBOSYLFORMIGLYCIAMMIDIME CYCLO-LICASE PRECURSOR (EC 6.3.3.1)
PHOSPHORIBOSYLFAMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE).
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CHAIN
SEQUENCE FROM N.A.

STRAIN-CV. VITA 3; TISSUE-ROOT NODULES;

SMITH P.M.C., MANN A.J., HALL D.J., ATKINS C.A.;

SMITH P.M.C., MANN A.J., HALL D.J., ATKINS C.A.;

Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.

-i- CATALYTIC ACTIVITY: ATP + 5'-PHOSPHORIBOSYL-FORMYLGLYCINAMIDINE

-i- PATHWAY: FIFTH STEP IN DE NOVO PURINE BIOSYNTHESIS.

-i- SUBCELLULAR LOCATION: CHLOROPLAST.
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REPEAT
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Vigna unguiculata (Cowpea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatrophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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l Similarity 80.
12; Conservative
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CYTOPLASMIC
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PROSITE; PS
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P24131;
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NUCLEOPHILE (BY SIMILARITY).
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STRAIN-NCIB 2951;
MEDLINE; 91216979.
HANCOCK K D
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                                                                                                       EMBL; M35107; AAA23216.1;
PIR; A39405; A39405.
                                                                                                                                                                                                                                                                                                  beta-galactosidase gene cloned in Escherichia coli
J. Bacteriol. 173:3084-3095(1991).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NO.
GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-I- INDUCTION: LATE IN THE ABE (ACETONE, BUTANOL, ERRMENTATION AND SUBJECT TO GLUCOSE REPRESSION
-I- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91216
HANCOCK K.R.,
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9; Conservative
'00703; Glyco_hydro_2; l.
ps00719; GLYCOSYL_HYDROL_F2_1;
ps00508; GLYCOSYL_HYDROL_F2_2;
e; Glycosidase.
e; Glycosidase.
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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alternative splicing, and polymorphisms.";
Genomics 52:312-324(1998).
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KRUGER W.D., COX D.R.;
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DE FRANCHIS R., MACLEAN K.N., BAO L., BUKOVSKA
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MEDLINE; 96057367.

SPERANDEO M.P., PHNICO M., PEPE A., CANDITO KRAUS J.P., ANDRIA G., SEBASTIO G.;

"Molecular analysis of patients affected by cystathionine beta-synthase deficiency: repo
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MEDLINE;
SEBASTIO
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KRUGER W.D., COX D.R.;

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"Hum. Mol. Genet. 4:1155-1161(1995).
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KLUIJTMANS
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Hum. Genet. 96:249-250(1995).
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mutations.";
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homocystinuria.";
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KOZICH V., KRAUS J.P.;

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HU F.L., GU Z., KOZICH V., KRAUS J.P., RAMESH V., SHIH V.E.

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"Two novel mutations (K384E and L539S)
cystathionine beta-synthase protein in
responsive homocystinuria patients.";
Hum. Mutat. 9:81-82(1997).
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modified and this statement is not remov-
entitles requires a license agreement (So-
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                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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PATHWAY: FIRST STEP IN HOMOCYSTEINE
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X82167; AAA98524 1; -...
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Metab. Dis. 18:211-214(1995).
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P.,
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Bioinformatics and the EMBL outstation -
titute. There are no restrictions on its
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NGUYEN T.D., CHEN P., F
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"Gene structure and pro
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 VARIANTS JC
MEDLINE; 98
SUZUKI Y.,
"Mutations
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                                                                            SEQUENCE FROM N.A.
MEDLINE; 98217378.
FINGERT J.H., YING L., SWIDERSKI R.E.,
ALWARD W.L.M., SHEFFIELD V.C., STONE E.
"Characterization and comparison of the
                                                                                                                                                                                                         TISSUE-LEUKOCYTE;
GARCHON H.-J.;
                                                                                                                                                                                                                                                      and chromosomal mapping.";
Genomics 41:360-369(1997).
                                                                                                                                                                                                                                                                           KUBOTA R., NODA S., WANG Y., MASHIMA Y., OGUCHI Y., SHIMIZ "A novel myosin-like protein cilium of the photoreceptor:
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MEDLINE; 97424389.
ORTEGO J., ESCRIBANO J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein cells.";
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Eukaryota; Metazoa; C
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MYCCILIN PRECURSOR (TRABECULAR
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EDLINE; 97312692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                                                                                                      GO J., ESCRIBANO J., COCA-PRADOS M.; ning and characterization of subtracted cDNAs from a human ary body library encoding TIGR, a protein involved in juven angle glaucoma with homology to myosin and olfactomedin." Lett. 413:349-353(1997).
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(., SHIRATO S.,
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                                   JOAG ARG-367
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                                                          8:377-384(1998).
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38, Last annotation update)
(TRABECULAR MESHWORK-INDUCED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., HUANG W.D., CHEN H., JOHNSON D., POLANSKY J.R.; properties of TIGR, an olfactomedin-related from glucocorticoid-induced trabecular meshwork
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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MANSERGH F.C., KENNA P.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glaucoma.
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STOILOVA D., CHILD A., BRICE G., CRICK R.P., FLECK B.W., SARFARAZI M.; "Identification of a new 'TIGR' mutation in a family with juvenile-onset primary open angle glaucoma."; ophthalmic Genet. 18:109-118(1997).
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"Recurrent mutations in a single exon encoding the evolutionarily conserved olfactomedin-homology domain of TIGR in familial open-angle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS JOAG ARG-367 AND LEU-370 MEDLINE; 98141135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAM M.F., BELMOUDEN A., BINISTI P., BREZIN A.P., VALTOT F., BECHETOILLE A., DASCOTTE J.-C., COPIN B., GOMEZ L., CHAVENTRE A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS POAG ARG-246; MEDLINE; 97472461.
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Am. J. Hum. Genet.
[9]
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                                                                                                                                                                                                                        DISEASE: DEFECTS IN MYOC ARE A CAUSE OF THE PRIMARY OPEN ANGLE GLAUCOMA (POAG). POAG IS SUBDIVIDED INTO TWO DIFFERENT CATEGORIES DEPENDING ON THE AGE OF ONSET: JUVENILE ONSET OPEN ANGLE GLAUCOMA (JOAG OR GLC1A) AND CHRONIC OPEN ANGLE GLAUCOMA (COAG) WHICH IS LATER IN ONSET. POAG IS A HIGHLY PREVALENT CAUSE OF IRREVERSIBLE BLINDNESS. IT IS CHARACTERIZED BY CUPPING OF THE OPTIC DISK AND ALTERATION OF THE VISUAL FIELD. BLEVATION OF INTRACCULAR PRESSURE IS OFTEN PRESENT AND IS A MAJOR RISK FACTOR. THE DISEASE IS PAINLESS AND OFTEN DIAGNOSED AT A LATE STAGE, WHEN VISUAL FIELD.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: EXPRESSED IN LARGE AMOUNTS IN VARIOUS TYPES OF MUSCLE, CILLARY BODY, PAPILLARY SPHINCTER, SKELETAL MUSCLE, HEART AND OTHER TISSUES. EXPRESSED PREDOMINAUTLY IN THE RETINA. IN NORMAL EYES, FOUND IN THE INNER UVEAL MESHWORK REGION AND THE ANTERIOR PORTION OF THE MESHWORK. IN CONTRAST, IN MANY GLAUCOMATOUS EYES, IT IS FOUND IN MORE REGIONS OF THE MESHWORK AND APPEARED MORE INTENSIFULY THAN IN NORMAL EYES, REGARDLESS OF THE TYPE OR CLINICAL SEVERITY OF GLAUCOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: LOCATED PREFERENTIALLY IN THE CILIARY ROOTLET AND BASAL BODY OF THE CONNECTING CILIUM OF PHOTORECEPTOR CELLS, AND IN THE ROUGH ENDOPLASMIC RETICULUM. ALSO SECRETED. ALTERNATIVE PRODUCTS: THE SHORT FORM MAY BE THE PRODUCT OF AN ALTERNATIVE INITIATION AT MET-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MAY PARTICIPATE IN THE OBSTRUCTION OF FLUID OUTFLOW THE TRABECULAR MESHWORK. \dot{\phantom{M}}
                                                                                                                                                                                    SIMILARITY: BELONGS TO THE OLFACTOMEDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            MODIFICATIONS
                                                                                                                                                                                                          DEFECTS ARE SEVERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet. 102:103-106(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6:2091-2097(1997).
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Best Local Similarity
Matches 8; Conser
SEQUENCE FROM N.A.

I S., KUSKE J., "SPURLOCK M.E.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-I- CATALYTIC ACTIVITY: (S)-3-HYDROXY-3-METHYLGLUTARYL-COA = ACETYL-COA + ACETOACETATE.
                                                                                                                                                                                BOVIN
8
                                                                                                                                                            HMGL_BOVIN Q29448;
                                                                  Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA LYASE (EC 4.1.3.4) (HMG-COA LYASE) (HL)
HYDROXY-3-METHYLGLUTARATE-COA LYASE) (FRAGMENT)
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                                                            Bovinae;
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AF049791; AAC14264.1; JOINED
AF049792; AAC14264.1; JOINED
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I -> F (IN COAG).

/FTId-VAR_005477.

1, 1919A632 CRC32;
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/FTId-VAR_005470.
G -> R (IN COAG).
/FTId-VAR_005471.
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/FTId=VAR_005469.
G -> V (IN JOAG).
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/FTId-VAR_005475.
N -> K (IN JOAG AND COAG).
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G -> R (II
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COILED COIL (POTENTIAL)
OLFACTOMEDIN-LIKE.
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V -> F (IN JOAG)
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I -> S (IN JOAG)
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Y -> H (IN JOAG)
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                                                                        Bovoidea; Bovidae;
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the Euro
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SEQUENCE
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PFAM;
PROSIT
                                                                                                                                             This
                                                                                                                                                                                                                                                                                                              TISSUE-LIVER;
93179448.
MITCHELL 6.A., ROBERT M.-F.,
BEHNKE C.E., MENDE-MUELLER L.
                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phas:
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA LYASE (EC 4.1.3.4)
HYDROXY-3-METHYLGLUTARATE-COA LYASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as lon modified and this statement is not removentified requires a license agreement (S or send an email to license@isb-sib.ch)
                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                         "3-hydroxy-3-methylglutaryl and chicken liver HL cDNAs a
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF
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                                                                                                                                                                                                                                                 J. Biol.
                                                                                                                                                                                                                                                                human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HMGL_CHICK P35915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM EDUROPEAN BIOINFORMATICS. Institute. There are no restrictly py non-profit institutions as long as its content.
                                                                                                                                                                                                      Biol. Chem. 268.4376-4381(1993).
CATALYTIC ACTIVITY: (S)-3-HYDROXY-3-METHYLGLUTARYL-COA
ACETYL-COA + ACETOACETATE.
PATHWAY: FINAL STEP OF KETOGENESIS AND LEUCINE CATABOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: FINAL STEP OF KETOGENESIS AND LEUCINE SUBUNIT: HOMODIMER (BY SIMILARITY). SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. SIMILARITY: BELONGS TO THE HMG-COA LYASE FAMILY
                                                                                                                                                                                            PATHWAY: FINAL STEI
SUBUNIT: HOMODIMER
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B45470; B45470.
; PF00682; HMGL-11)
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                                                                                                                                                                                                                                                                                                                                                                                             data; Craniata; Vertebrata; Phasianidae; Phasianidae;
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                                       ALT
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Pred. No. 6.1;
5; Mismatches
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5.1;
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                                                                           http://www.isb
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EE C., GIBSON
                                                                                                                                                                                                                                                                           Cloning of a mutation
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Gallus.
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RESULT 10
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Matches
EMBL; U49878; A
EMBL; U49871; A
EMBL; U49871; A
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EMBL; U49873; A
EMBL; U49876; A
EMBL; U49876; A
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EMBL; U49876; A
EMBL; U49878; 
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MEDLINE; 9336,
WANG S., NADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyase; Mitochondrion ACT_SITE 239 2: SEQUENCE 298 AA;
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIM-129.
MEDLINE; 96207305.
WANG S.P., ROBERT M.-F., GIBSON K.M., WANDERS R.J.A., "3-hydroxy-3-methylglutaryl CoA lyase (HL): mouse and (HMGCL) cloning and detection of large gene deletions unrelated HL-deficient patients.";
Genomics 33:99-104(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA LYASE, MITOCHONDRIAL PRECURSOR (EC)
(HMG-COA LYASE) (HL) (3-HYDROXY-3-METHYLGLUTARATE-COA LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..... NADEAU J.H., DUNCAN A., ROBERT M.-F., FONTAINE G.,
SCHAPPERT K., JOHNSON K.R., ZIETKIEWICZ E., HRUZ P., MIZIORKO H.;
"3-hydroxy-3-methylglutaryl coenzyme A lyase (HL): cloning and
characterization of a mouse liver HL cDNA and subchromosomal mapping
of the human and mouse HL genes.";
Mamm. Genome 4:382-387(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P38060;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: MITOCHONDRIAL SIMILARITY: BELONGS TO THE HMG-COA I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYL-COA + ACETOACETATE.
PATHWAY: FINAL STEP OF KETOGENESIS AND SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 42.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A
                                            AAB03107.
AAB03107.
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AAB03107.1;
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31436 MW;
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42.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
A2EE0702 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYASE
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Mus.
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human HL
in two
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                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration - MBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                               outstation
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ACT_SITE
CONFLICT
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SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMGL_RAT P97519;
                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: FINAL STEP OF KETOGENESIS AND LEUCINE CATABOLISM.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                        CULLINGFORD T.E., DOLPHIN C.T., CANEVARI L., CLARK J.B.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-:- CATALYIC ACTIVITY: (S)-3-HYDROXY-3-METHYLGLUTARYL-COA -
ACETYL-COA + ACETOACETATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-VUL-1999 (Rel. 38, Last annotation update)
15-VUL-1999 (Rel. 38, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA LYASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.
(HMG-COA LYASE) (HL) (3-HYDROXY-3-METHYLGLUTARATE-COA LYASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyase;
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                      Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                        !- SIMILARITY: BELONGS TO THE HMG-COA LYASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                     1 ATOKITYRISGVGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATEDLVYMLNGLGI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATQKITYRISGVGI
ATEDLVYMLTGLGI 290
                                                                                                                                                                            Y10054; CAA71148.1; -. PF00682; HMGL-like; 1.
                                                                                                                                          Mitochondrion; 27
                                            Similarity 42. 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                    PS01062; HMG_COA_LYASE; 1.
                                                                                                  28
266
325
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62
231
238
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                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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266
34192
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325
266
63
1
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238
34161 MW;
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                                                      51.4%;
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                                                                                                    t peptide.
MITOCHORION (BY SIMILARITY).
HYDROXYMETHYLGLUTARYL-COA LYASE.
BY SIMILARITY.
; C68DE719 CRC32;
                                                        Score 38; DB 1;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N -> K (IN REF. 2).
G -> A (IN REF. 2).
I -> Y (IN REF. 2).
3448C502 CRC32;
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                                                                  Length 325;
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                                            Indels
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3_MOUSE
TSP3_MOUSE
Q05895;
Q1-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the comp
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I SUBUNIT: OLIGOMER, CROSS-LINKED BY DISULFIDE BONDS.

I TISSUE SPECIFICITY: BRAIN, LUNGS AND CRATTILAGE.

I SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.

I SIMILARITY: CONTAINS 7 TYPE-3 TSP REPEATS (WHICH BIND CALCIUM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DUHIG T., GENDLER S.J., BORNSTEIN P.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ADHESIVE GLYCOPROTEEN THAT MEDIATES CELL-TO-CELL
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-B6/CBA; TISSUE-LUNG;
MEDLINE; 93224149.
BORNSTEIN P., DEVARAYALU S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Creat
01-JUN-1994 (Rel. 29, Last
01-OCT-1996 (Rel. 34, Last
THROMBOSPONDIN 3 PRECURSOR.
                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C;
VOS H.L., MOCKINGSTURM-WILSON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Thrombospondin 3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THBS3 OR TSP3
                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 834-956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE; 92291102.
VOS H.L., DEVARAYALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOS H.L., DEVARAYALU S., DE VRIES Y., "Thrombospondin 3 (Thbs3), a new membe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 517-956 FROM N.A.
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A46016;
A44124;
                                                                                                                                                                                                                                                                                                                                                                                         L24434;
M86620;
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d characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267:12192-12196(1992).
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    Created)
    Last sequence update)
    Last annotation update)

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Eutheria; Rodentia;
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EGF-LIKE 3, CALCIUM-BIND
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MEDLINE; 92283859.
SWAROOP M., BRADLEY K., OHURA T., TAHARA ROSENBERG L.E., KRAUS J.P.;
"Rat cystathionine beta-synthase. Gene or splicing.";
J. Biol. Chem. 267:11455-11461(1992).
                                                                                                                                                                                                                                                               EMBL; M88344; AAB02042.1; -. EMBL; M88346; AAA42024.1; -. EMBL; D01098; BAA00883.1; -. PIR; JX0145; JX0145. PIR; A42790; A42790. PFAM; PF00291; S_T_dehydratase PFAM; PF00571; CBS; 1.
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J. Biochem. 108:899-902(1990)
-!- CATALYTIC ACTIVITY: L-SER
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STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
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SUBCELLULAR LOCATION: CYTOPLASMIC.
ALTERNATIVE PRODUCTS: FOUR VARIANTS CAN BE FORMED BY ALTERNATIVE
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TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, AND BRAIN.
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                                                                                                                                                                                                                                                                                                                                                      **COMPLETE ADDISCHMIDT M.D., WALSH M.J., ZIMBELMANN R., FRANKE W.W

"Complete amino acid sequence of the epidermal desmoglein precurso.

polypeptide and identification of a second type of desmoglein gene

EUR. J. Cell Biol. 55:200-208(1991).

1- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.

1 INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIAT

FILAMENTS MEDIATING CELL-CELL ADHESION.

1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

1- TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINOMAS.

1- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92
KOCH P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1997 (Rel.
                                                                                                                                                                                                                                 EMBL: Z26317; CAA81226.1;
HSSP; P15116; INCI.
MIM: 125671; -.
                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of the ubiquitous human desmoglein, Dsg2, and expression catalogue of the desmoglein subfamily of desmosomal
                                                                                                                                                               DOMAIN
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Q14126;
        SEQUENCE
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                                                                                                                                                                                                 Cytoskeleton;
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SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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"HMG COA lyase deficiency:
mutations in codons 41 and
mutation, R410.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS HMG GLN-41; GLU-42; GLY-42
MEDLINE; 98130531.
MITCHELL G.A., OZAND P.T., ROBERT M.
GIBSON K.M., WANDERS R.J., WANG S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBERTS J., MITCHELL G.A., MIZIORKO H.M.;
"Modeling of mutatino responsible for human 3-hydroxy-3-
methylglutaryl-CoA lyase deficiency implicates histidine-233
active site residue.";
J. Biol. Chem. 271:24604-24609(1996).
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MEDLINE; 93179448.
MITCHELL G.A., ROBERT M.-F.,
BEHNKE C.E., MENDE-MUELLER L.
MIZIORKO H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Furtheria; Primates; Catarrhini; Hominidae; Homo.
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WANG S.P., ROBERT M.-F., GIBSON K.M., WANDERS R.J.A., ""3-Hydroxy-3-methylglutaryl CoA lyase (HL): mouse and "13-Hydroxy-3-methylglutaryl CoA lyase (HL): mouse and (HMGCI) cloning and detection of large gene deletions unrelated HL-deficient parients."; Genomics 33:99-104(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WARIANT HMG ARG-233.
MEDLINE: 96394619.
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PATHWAY: FINAL STEP OF KETOGENESIS AND LEUCINE CATABOLIS SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
TISSUE SPECIFICITY: FIBROBLASTS, LIVER AND LYMPHOBLASTS.
TISSUE SPECIFICITY: FIBROBLASTS, LIVER AND LYMPHOBLASTS.
DISEASE NOWN AS HYDROXYMETHYLGLUTARICACIDURIA (HMG) WHI
DISEASE KNOWN AS HYDROXYMETHYLGLUTARICACIDURIA (HMG) WHI
LEAD TO HYPOGLYCEMIA AND COMA.
SIMILARITY: BELONGS TO THE HMG-COA LYASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       J. Hum. Genet. 62:295-300(1998).
CATALYTIC ACTIVITY: (S)-3-HYDROXY-3-METHYLGLUTARYL-COA - ACETYL-COA + ACETOACETATE.
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                                                                                                                                                                                                                                                                                                                                                                        LEUCINE CATABOLISM
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A (HMG) WHICH CAN
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SWISS-PROT entry is copyright. It is produced through a collaboration -

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Query Match 50.0%; Score 37; DB 1; Best Local Similarity 42.9%; Pred. No. 21; Matches 6; Conservative 4; Mismatches
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EMBL; U49719; F
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EMBL; U49714; F
EMBL; U49716; F
EMBL; U49716; F
EMBL; U49717; F
                                                                                                                                               CONFLICT
SEQUENCE
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VARIANT
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PS01062; HMG_COA_LYASE; 1.
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325 AA; 34390 MW;
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D -> E (IN HMG).

FTIG-VAR_003745.
D -> G (IN HMG).

FTIG-VAR_003746.
D -> H (IN HMG).

FTIG-VAR_003747.
V -> L (IN HMG).

FTIG-VAR_003748.
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T -> A (IN REF. 2).
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Search completed: January 7, 2000; 13:25:35 Job time: 387 sec ₽ **%** 

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ISHIKAMA H., LI K., UITTO J.;

Submitted (JAN-1997) to the EMBL/.

-I- SUBCELLULAR LOCATION: TYPE I

EMBL; U86016; AAB65091.1; -

PFAM; PF00028; cadherin; 4.

PROSITE; PS00232; CADHERIN; 2.

Cell adhesion; Glycoprotein; Tran

Cell adhesion; Glycoprotein; Tran
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    Transmembrane; Calcium-binding;

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Best Local S
Matches 7
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Best Local (
O22282 PRELIMINARY; PRT; 441 AA.
O22282;
O1-AN-1998 (TIEMBLrel. 05, Created)
O1-JAN-1998 (TIEMBLrel. 05, Last sequence update)
O1-JUN-1998 (TIEMBLrel. 06, Last annotation update)
T517.1 PROTEIN.
T517.1 OR F17A14.8.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; euphyllophytes; Spermatophyta; Magnollophyta; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
01-NOV-1996
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                              1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1453
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Development 125:4055-4066(1998).
EMBL; AF079764; AAC64271.1; ...
SEQUENCE 2023 AA; 220680 MW: 10700007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLARK H.F., BRENTRUP D., SCHNEITZ K., BIEBER A., GOODMY Dachsous encodes a member of the cadherin superfamily imaginal disc morphogenesis in Drosophila."; Genes Dev. 9:1530-1542(1995).

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SEMBL; LO8811; AAA79329:1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 98407961.
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TMAGINAL DISC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 58. 7; Conservative
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7; Conserv
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Pred. No. 4.4e+02;
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Pred. No. 1.6e+02;
3; Mismatches 4
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Best Local Similarity 54.
Matches 6; Conservative
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O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JAN-1998 (TrEMBLrel. 07, Last annotation update)
O1-AUG-1998 (TrEMBLrel. 07, Last annotation update)
UVDOTHETICAL 15.6 KD PROTEIN.
066968;
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MEDLINE: 98037514.

MITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE.H.-M., DUBOIS ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K., ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K., HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., SPADAFORA R., VICARE R., MANG Y., WIERZBOWSKI J., GIBSON R., JUNION R., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S., MCDUGALL S., SHAWER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics."; Bacteriol. 179:7135-7155(1997).
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ROUNSLEY S.D., LLN., KETCHUM K.A., CROSBY M.L., BRANDC
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS N
SOMERVILLE C.R., VENTER J.C.;
SUBMILTED (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003000; AAB87120.1;
EMBL; AC003674; AAB97126.1;
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ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDC
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M
SOMERVILLE C.R., VENTER J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum Archaea; Euryarchaeota; Methanobacte
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8; Conserv
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147 AA; 15626 MW;
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                               PRELIMINARY;
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Best Local S
Matches 7
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01-AUG-1998 (TYEMBLIE). 07, Last s
01-AAY-1999 (TYEMBLIE). 10, Last a
PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
Lyase.
ACT_SITE
SEQUENCE
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BALTSCHEFFSKY M., BROSCHE M., HULTMAN T., SAKAI-NORE Y., SEVERIN A., STRID A.;

"A 3-hydroxy-3-methylglutaryl-CoA lyase ge bacterium Rhodospirilium rubrum.";

B10chim. B1ophys. Acta 1337:113-122(1997).
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01-MAY-1997 (TIEMBLIEL 03, Last sequence update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA LYASE (EC 4.1.3.4) (HMG-COA
(3-HYDROXY-3-METHYLGLUTARATE-COA LYASE)
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Bacteria; Aquificales;
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                                                                                                               PROSITE;
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                                                                                                                                                         (S)-3-HYDROXY-3-METHYLGLUTARYL-COA-
SIMILARITY TO OTHER SPECIES HMG-COA
L; U41280; AAB50182-1; --
M; PF00682; HMGL-11ke; 1
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239
303 1
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                                                                                                                   HMG_COA_LYASE;
239
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SNEAD M.A., KELLER M., AU
OLSON G.J., SWANSON R.V.;
e EMBL/GenBank/DDBJ datab
    ME;
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SIMILARITY.
44C2DA4B CRC32;
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annotation update)
E CYCLO-LIGASE.
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LYASE.
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HUBER
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Query Match

Score

38;

DB

2

Length

Query Match Best Local S Matches

Similarity 88. 8; Conservative

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Submitted (JAN-1998) to the
EMBL; X96770; CAA65545.1;
EMBL; Z73504; CAA97853.1;
EMBL; X16253; CAA76138.1;
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01-JUN-1996
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Q12036;
                                                                                                                                                                                                                                                                               SEQUENCE FROSTRAIN-3D7;
                                                                                                                                 HAMLIN N., LAWSON D., BARRELL B.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ
EMBL; AL008970; CAA15615.1; -.
PFAM; PF00271; helicase_C; 1.
SEQUENCE 2269 AA; 267233 MW; 11E1C8E0 CRC:
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01-MAY-1999
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SEQUENCE 1
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PURNELLE B.,
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Sukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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(JUN-1996)
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MEDLINE: 98315113.

MALAGA-TRILLO E., MCANDREW B., V SUBLIMANN H., FIGUEROA F., KLEIN "Linkage relationships and haple (class II B loci.", Genetics 149:1527-1547(1998).

EMBL: AF049971; AAC41310.1; -. PFAM; PF00969; MHC_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 10, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS II B LOCUS 4 (FRAGMENT).
07-eochromis niloticus (Nile tilapia) (Tilapia nilotica).
07-eochromis niloticus (Nile tilapia) (Tilapia nilotica).
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07-eochromis niloticus (Nile tilapia) (Tilapia).
08-eochromis niloticus (Nile tilapia) (Tilapia).
09-eochromis niloticus (Nile tilapia) (Tilapia).
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BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAITEILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAITEILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORRIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
EMBL: Z50177; CAA90547.1;
SEQUENCE 287 AA; 32464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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SEQUENCING PROJECT, ESSA;
EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ
EMBL; 297338; CAB10302.1;
PFAM; PF00005; ABC_tran; 1.

SEQUENCE 1177 AA; 134263 MW; 32946ADC CRC3
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                                                                                                                                                  Arabidopsis tihaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Eukaryota; Viridiplantae; Streobyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streobyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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7; Conser
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398 (TIEMBLrel. 08, Last sequence update)
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399 (TIEMBLrel. 10, Last annotation update)
HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR.
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Pred. No. 9.8;
3; Mismatches
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Pred. No. 2e+02;
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Q92566;
01-FEB-1997
01-FEB-1997
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DODSON R., GWINN M., F
SODERGREN E., HARDHAM
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AE001251; AAC65775.1; -. PFAM; PF01368; DHH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999)
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377 ATEDVVYMLNGLGV 390
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SEQUENCE 240
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PFAM; PF00028; cadherin; 5.
PFAM; PF00008; EGF; 6.
PFAM; PF00004; laminin_G; 1.
PROSITE; PS00232; CADHERIN;
                                                                                                                                                                                                                                      DNA Res. 3:321-329(1996).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                           The coding sequences of analysis of cDNA clones DNA Res. 3:321-329(1996)
                                                                                                                                                                                                                                                                                        NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARABAN
TANAKA A., KOTANI H., MIYAJIMA N., NOMURA N.;
"Prediction of the coding sequences of unidentified
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Me
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                                                                                                                                                                                                                                                                                                                            MEDLINE;
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                                                                                                 Score 37; DB Pred. No. 6.9e 4; Mismatches
                                                                                                                                                                              Transmembrane; Calcium-binding; Repeat.
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6.9e+02;
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 6, 2000, 15:40:34; Search time 51.33 Seconds (without alignments) 6.922 Million cell updates/sec

Title:
Perfect score:
Sequence: US-08-991-628-2 78 1 FGIFVVDKNTGDINI 15

Scoring table: BLOSUM62

Searched:

188963 seqs, 23686106 residues

Database : A\_Geneseq\_36:\*

Word size : 0

Number of hits that pass the threshold :

188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	22 22 23 24 25 25 26 27 27 27 27 27 27 27 27 27 27 27 27 27	9 11 11 13 14 11 16 11 10 11 10 11 10 11 11 11 11 11 11 11	Result NO. 1 2 3 4 4 6 6
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07-MAR-1996; US-400796.
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(HARD) HARVARD COLLEGE
Strominger JL, Wucherpfennig K
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30-JUN-1995; 165632.
30-JUN-1994; JP-173291.
(NISH/) NISHUKAWA T.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Self epitope of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HA, human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W04842 standard; peptide; 15 W04842;
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Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for
                                                                                                                                                                                                                                                                                                                                  WO9627387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
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R93962 standard;

peptide;

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05-JUL-1996 (first entry)
Peptide combining with anti-interepidermal cellular antibody anti-interepidermal cellular antibody; adsorber

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DR MPI; 96-045392/05.

Pr Anti-Interepldermal cellular antibody-combining peptide - which can per be immobilised on column to form adsorbent useful for treating diseases related to the antibody related to the antibody related to the antibody related to the antibody related to the sequence valual aspectife for properties are disclosed which contain at least 5 contiguous amino acids from the sequence valual spile aspectife properties are disclosed which containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
                                                   Query Match
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Matches 12
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Peptide combining with anti-interepidermal cellular antibody
anti-interepidermal cellular antibody; autoantibody; adsorbe
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J07309893-
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28-NOV-1995.
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                                                                                                                                                                                                                                     I Franke WW, Schafer S;

N WPI; 97-146518/14.

Antibody reactive with part of desmosomal cadherin - exposed on PT surface of epithelial or carcinoma cells, not bound to desmosomes, PT surface of epithelial or carcinoma cells, not bound to desmosomes, PT useful for diagnosis and treatment of carcinoma micrometastases PS Claim 7; Page 5; Bpp; German.

CC desmoglein begg, which is exposed on the surface of epithelial or CC carcinoma cells and not bound to desmosomes. An antibody (Ab) CC directed against epitopes of the present sequence can be used to CC diagnose, i.e. to detect carcinoma cells, especially comicrometastases, not bound to desmosomes. An antibody and CC datect living or fixed carcinoma cells by cell sorting methods and CC as a therapeutic to deliver agents, e.g. other Ab or toxins, to CC carcinoma cells. The Ab provides rapid and reliable detection of constants of carcinoma. And detects parts of DC that are not
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Best Local Similarity 100
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New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile Thr Alla Ile Val Asp Arg Glu Glu (see R93960), the peptide not containing more than 50 residues. The peptide combines with anti-interepidermal cellular antibody. It can be immobilised on a carrier to prepare an absorbent useful for the treatment of diseases related to anti-interepidermal cellular antibody. The present sequence is a specific example of the new peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
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18-MAY-1994; 129556
18-MAY-1994; JP-129
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23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK
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Best Local s
Matches
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P-PSDB; 766428.

Pemphigus foliaceus antigen-IgG constant region fusion protein - lini through the hinge region used to treat pemphigus foliaceus (laim 1, page 10-12; 17pg; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus antigen protein through the hinge portion. Pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiormis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is protein is useful to treat pemphigus foliaceus.
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25-MAR-1997.
12-SEP-1995;
12-SEP-1995;
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J07309893-A:
28-NOV-1995.
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pemphigus foliaceus; autoantibody; constant region 
extracellular region; antigen; hinge portion; sk 
dermatitis herpetiformis; fusion protein; detect
Anti-interepidermal cellular antibody-combining peptide - which can be immobilised on column to form adsorbent useful for treating diseases related to the antibody.

Example 3; Page 5; 7pp; Japanese.

New peptides are disclosed which contain at least 5 contiguous amino acids from the sequence Val Gly Ile Asp Gln Pro Pro Phe Gly Ile Phe Val Val Asp Tys Asn Thr Gly Asp Ile Asn Ile Thr Alla Ile Val Asp Arg Glu Glu (see R93960), the peptide not containing more than 50 residue The peptide combines with anti-interepidermal cellular antibody. It
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in immunodiagnosis.
Sequence 778 AA;
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18-MAY-1994; JP-129556.
(KURS ) KURARAY CO LTD.
WPI; 96-045392/05.
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Peptide combining with anti-interepidermal cellular antibody
anti-interepidermal cellular antibody; autoantibody; adsorber
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05-JUL-1996
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Best Local
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The present sequence is full length human cadherin-13, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA is a solated from a foetal brain cDNA library, using probes based on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 713 AA;
                                                                                                                                                                                                                     Human cadherin-13
Human; cadherin; 1
superfamily; cyto:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Full length human cadherin-13.
Ca2+ dependent; cell adhesion protein; foetal; cadherin; brain; human; antibody; purification; determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present Sequence 1
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                    08-JUL-1997.
17-APR-1992; 872643.
19-APR-1993; US-049460
                                                                                                US5646250-A.
                                                                                                                                                Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 97-108328/10.
N-PSDB; T61927.
                                                                                                                                                                                                                                                                                  03-NOV-1997 (first entry)
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17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
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JS5597725-A.
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                                                                                                                                                                                                                                                                                                                                     v25638 standard; Protein;
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cytoskeleton; eatenin; cancer.
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FI Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
CC This sequence represents human cadherin-13. The invention specifically
CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat
CC cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell
CC adherin-8 red in the part of the cadherin proteins. They are glycosylated integral membrane proteins
CC that have an N-terminal extracellular domain that determines binding
CC specificity, a hydrophobic membrane spanning region and a C-terminal
CC specificity, a hydrophobic membrane spanning region and a C-terminal
CC cytoplasmic domain, which is highly conserved among members of the
CC superfamily. The C-terminal domain interacts with the cytoskeleton
CC novel cadherin sand other cytoskeleton-associated proteins. The
CC cadherins in various cancers. Sequence analysis of the cadherin
CC cadherins in various cancers. Sequence analysis of the cadherin
CC cadherins in various cancers. Sequence analysis of the cadherin
CC cadherins also allows investigation of the structure and function of
CC cadherin. The cadherin proteins may be isolated by using anti-cadherin
CC cantibodies. These antibodies may also be used to modulate the activity
CC of cadherin and to determine the tissue specific distribution of cadherin
CC proteins. Each subclass of cadherins has a unique tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 6
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17-APR-1992; US-872643.
19-APR-1993; US-049460.
26-JAN-1994; US-188228.
(DOHE-) DOHENY EYE INST.
The present sequence is a putative human cadherin-12, which is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA was isolated from a foetal brain cDNA literary, using probes based on homologous rat cadherin cDNA.

Antibodies or fragments that specifically bind the human cadherin can be used to purify the cadherin, determine its tissue expression and antagonise its ligand/antiligand binding activities.

Sequence 794 AA;
                                                                                                                                                                                                                                                                                                       17-APR-1992; 19-APR-1993; 126-JAN-1994;
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Sequence
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N-PSDB; T61926.
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Ca2+ dependent; cell adhesion protein; foetal; cadhe
brain; human; antibody; purification; determination;
tissue expression; binding antagonist; calcium ion;
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01-NOV-1994;
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N-PSDB; T85405.
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6; Conserv
                                                                                                                                                                                                     to cadherin proteins - useful as cadherin antagonists,
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17-APR-1992; 872643.
19-APR-1993; US-049460.
17-APR-1992; US-872643.
01-NOV-1994; US-332638.
(DOHE) DOHENY EXE INST.
                                                                                                                                                                                                                                                                                                                                                                                                 adhesion proteins. They are glycosylated integral membrane proteins that have an N-terminal extracellular domain that determines binding specificity, a hydrophobic membrane spanning region and a C-terminal cytoplasmic domain, which is highly conserved among members of the superfamily. The C-terminal domain interacts with the cytoskeleton through eatenins and other cytoskeleton-associated proteins. The novel cadherin proteins may be used in the analysis of the role of cadherins in various cancers. Sequence analysis of the cadherin proteins also allows investigation of the structure and function of cadherin. These antibodies may be isolated by using anti-cadherin antibodies. These antibodies may also be used to modulate the activity of cadherin and to determine the tissue specific distribution of cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T85404.

Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion Claim 1; Column 95-100; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents human cadherin-12. Tprovides details of human cadherin-5, -8, -11,
                                         Alpha 6B integrin subunit.

Human; alpha 6A; alpha 6B; integrin; cell surface receptor; adhesion; extracellular matrix; cytoskeleton; heterodimer; laminin receptor; immunoprecipitation; JAR; choriocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cadherin-8, -5, -11 and -13. Cadherins are calcium-dependent cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5646250-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      superfamily; cytoskeleton; eatenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cadherin; rat; calcium-dependent cell adhesion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cadherin-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W25637 standard;
                                                                                                                     R28822 standard; Protein; 1091 AA. R28822;
                                                                                                        23-MAR-1993 (first entry)
                             iomo sapiens
                                                                                                                                                                                                                   101 VFTIDETTGDIH 112
                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 794 AA
Location/Qualifiers 1012. .1037
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                                                                                                                                                                                                                                                                                                           Length 794;
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binding to various extracellular components. Each integrin receptor is a heterodimer comprised of an alpha and a beta subunit. Each alpha subunit tends to associate with only one type of beta subunit but there are several exceptions to this rule. These integrins correspond to the laminin receptor. The cytoplasmic domain of the 6A and 6B integrins differs from previously isolated alpha 6 integrins. The human alpha 6B was isolated from human choriocarcinoma cell line JAR
                                                                                                                                        in body samples
Disclosure; Page 78-82; 115pp; English.
Disclosure; Page 78-82; 115pp; English.
The sequences given in R28821-22 are the human alpha 6A and 6B
Integrin subunits. Integrins are a family of cell surface receptors
Integrin subunits. Integrins are a family of cell surface receptors
which serve cellular adhesion functions. These receptors form a lin
which serve cellular matrix and the cytoskeleton through their
between the extracellular matrix and the cytoskeleton through their
between the extracellular matrix and the cytoskeleton through their
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Quaranta V, Tamura RN;
WPI; 92-398799/48.
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by immunoprecipitation studies. Sequence 1091 AA;
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US-695564.
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N. PSDB; Q65673.

Integrins are neterodimers comrised of alpha beta4 cell surface protein Example 5; Figure 6; 34pp; English.

Integrins are heterodimers comrised of alpha and beta subunits, that care non-covalently associated transmembrane glycoproteins. In alpha chains and 6 beta chains have been recognised in man. Each alpha subunit tends to associate with only one type of beta subunit but there are several exceptions. Integrins mediate (in part) the interaction of cells with the extracellular matrix, forming a link between the extracellular matrix and the cytoskeleton. They may transmit signals from the extracellular to the intracellular environment, affecting cell behaviour. This sequence is the alpha6 subunit of an alpha6 beta4 integrin.
                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
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19-FEB 1987; 016552.

19-FEB 1987; US-016552.

04-JAN 1989; US-293384.

01-OCT-1990; US-591105.

(KAJI/) KAJIJI S.

(QUARK) QUARANTA V.

KAJIJI S. QUARANTA V.

WPI; 94-191533/23.
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Alpha subunit of integrin cell surface receptor.
Alpha subunit of integrin cell surface receptor.
Integrin; alpha; beta; subunit; glycoprotein; heterodimer;
transmembrane; extracellular matrix; cell signalling; cytoskeleton;
behaviour; signal transduction; receptor.
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377 FGIAV--KNIGDIN 388
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/*tag- f
/*tos- "This sequence is conserved in all but the
Drosophila PS2 alpha subunit"
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/note= "Putative cation binding site."
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/note= "Putative cation binding site."
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cleavage site of other integrin O chains."
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desmoglein 2 - hum
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desmoglein 1 precu
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cadherin 7 - chick
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BH-protocadherin P
BH-protocadherin p
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K-cadherin - rat
cadherin-6B - chic
cadherin-14 - huma
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N;Alternate names: (
C;Species: Homo sapi
C;Date: 20-Feb-1995
C;Accession: S38673;
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S38673
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                                                    R;Zimbelmann,
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Best Local s
Matches 15
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Amagai, M.; Klaus-Kovtun, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
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15; Conserv
                                                                                                                   human
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Result

### ALIGNMENTS

Stanley,

J.R.

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A;Map position: 18q12.1-18q12.2

C;Superfamily: cadherin; cadherin repeat homology

C;Keywords: calcium binding; cell adhesion; duplication; gly:

F;1-23/Domain: signal sequence *status predicted <SIG>
F;24-49/Domain: propeptide *status predicted <PRO>
F;50-999/Product: deamoglein homolog *status predicted <MAT>
F;50-91/Promain: extracellular *status predicted <EXT>
F;50-615/Domain: cadherin repeat homology <CR1>
F;160-267/Domain: cadherin repeat homology <CR2>
F;270-383/Domain: cadherin repeat homology <CR3>
F;390-495/Domain: cadherin repeat homology <CR3>
F;496-598/Domain: cadherin repeat homology <CR3>
F;406-598/Domain: cadherin repeat homology <CR3>
F;406-598/Domain: cadherin repeat homology <CR3>
F;406-639/Domain: transmembrane *status predicted <INM>
F;610-639/Domain: intracellular *status predicted <INM>
F;610-999/Domain: intracellular *status predicted <INM>
F;610-999/Domain: intracellular *status predicted <INM>
submitted to the EMBL-Data A; Reference number: $38673 A; Accession: $38673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;910-938/Domain: desmoglein repeat <DG1>F;937-966/Domain: desmoglein repeat <DG2>F;110,180,545/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-999 <AMA>
A;Cross-references: GB:M76482; NID:g190751; PIDN:AAA60230.1; PID:g190752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, A;Reference number: A41088; MUID:92069753
A;Accession: A41088
                                                                                                                     Altérnate names: desmoglein HDGC (Species: Homo sapiens (man)
Date: 20-7eb-1995 #sequence_revision
Accession: S38673; B38872
                                                                                                                                                                                                                                                                                                                                                                                 FGIFVVDKNTGDINI 15.
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12.1-18q12.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78;
Pred. No.
                                                                  September 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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s 0;
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submitted to the EMBL Data A; Reference number: S16906
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A;Map position: 18q12.1-18q12.2
C;Superfamily: cadherin; cadherin repeat homology
C;Superfamily: calcium binding; cell adhesion; duplication; glycoprotein; membrane protein
F;51-158/Domain: cadherin repeat homology <CR1>
F;161-271/Domain: cadherin repeat homology <CR2>
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A; Residues: I-1117 <ZIM>
A; Cross-references: EMBL: Z26317; NID: 9416177;
A; Cross-references: EMBL: Z26317; NID: 9416177;
B; Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.;
Eur. J. Cell Biol. 55, 200-208, 1991
A; Title: Complete amino acid sequence of the e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1049 <BUX>
A; Residues: 1-1049 <BUX>
A; Coss: references: EMBL: X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
A; Cross: references: EMBL: X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
A; C.L.; Ataliotis, P.; Poynter, D.; Arnemann, J.; Proc. Natl. Acad. Sci. U.S.A. 88, 4796-4800, 1991
A; Title: Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, A; Reference number: A39706; MUID:91271279
A; Accession: A39706
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A;Cross-references: GDB:125563; OMIM:125670
A;Map position: 18q12.1-18q12.2
C;Superfamily: cadherin: cadherin repeat ho:
C;Keywords: calcium binding; cell adhesion;
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A;Accession: B38872
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A; Residues: 24-1049 < MHE>
A; Cross-references: GB:X56654
A; Cross-references: GB:X56654
CR: Milles, L.A.; Parry, D.A.D.;
J. Cell Sci. 99, 809-821, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Title: Structural analysis and expression of human desmoglein: a cadherin·like compone;Reference number: A61254; MUID:92121251
;Accession: A61254
                                                                                                                                                                                        ;Molecule type:
;Residues: 1-55
                                                                                                                                                                                                                  Status: not compared with conceptual translation; Molecule type: mRNA
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Residues: 26-1049 <NIL>
Wheeler, G.N.; Buxton, R.S.; Parker, A.E.; Arnemann, Iochem. Soc. Trans. 19, 1060-1064, 1991
Title: Desmosomal glycoproteins I, II and III: novel Reference number: A61279; MUID:92175187
Accession: A61279
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;Residues: 26-1049 <
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Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999;
Accession: S16906; A39706; A61254; A61279; S16158
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;Residues: 777-1117 <KOC>
;Cross-references: GB:S64273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Powers, E.E.; Angst, B.D.; Wagner, R.M.; Green,
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   repeat homology adhesion; duplication;
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Zimbelmann, R.; 1
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glycoprotein; transmembrane
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Franke, W.W.
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A;Title: Identification of desmoglein, a constitutive desmosomal glycoprotein, A;Reference number: A48173; MUID:91168965
A;Accession: A48173
                                                                        A;Molecule type: mRNA
A;Residues: 44-1043 <ZIM>
A;Residues: 44-1043 <ZIM>
A;Cross-references: EMBL:X57784; NID:g436061; PIDN:CAA40930.1; PID:g436062
A;Cross-references: EMBL:X57784; NID:g436061; PIDN:CAA40930.1; PID:g436062
R;Koch, P.J; Walsh, M.J; Schmelz, M.; Goldschmidt, M.D.; Zimbelmann, R.;
Eur. J. Cell Biol. 53, 1-12, 1990
Eur. J. Cell Biol. 53, 1-12, 1990
                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1991 A; Reference number: $38721 A; Accession: $38721
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:S64268; GB:S64270
R;Goodwin, L.; Hill, J.E.; Raynor, K.; Raszi, L.; Manabe, M.;
Biochen. Biophys. Res. Commun. 173, 1224-1230, 1990
A;Title: Desmoglein shows extensive homology to the cadherin A;Reference number: A37785; MUID:91097553
A;Accession: A37785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-1043 - KNCD-
A;Cross-references: EMBL:X58466; NID:g306; PIDN:CAA41380.1; PID:g307
A;Cross-references: EMBL:X58466; NID:g306; PIDN:CAA41380.1; PID:g307
A;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. 55, 200-208, 1991
A;Title: Complete amino acid sequence of the epidermal desmoglein precursor
A;Reference number: A38872; MUID:g2037656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bos primigenius taurus (cattle)
C;Date: 30. Jun-1993 #sequence_revision 30. Jun-1993 #text_change
C;Accession: S14603, A38872; A37785; S38721; A48173; S24412
R;Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W.
submitted to the EMBL Data Library, March 1991
A;Description: Complete sequence of the desmoglein precursor and A;Reference number: S14603
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A; Residues: 44-123, 'V', 125-493
A; Cross-references: GB: M58165;
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                                                                                                                                                                                                                                                                                                                                R; Zimbelmann,
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A; Residues: 1-87; 968-1043 < KO2>
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549-569/Domain: transmembrane #status predicted .

572-1049/Domain: intracellular #status predicted

840-869/Domain: desmoglein repeat <DG1>

870-899/Domain: desmoglein repeat <DG2>

900-927/Domain: desmoglein repeat <DG3>

928-956/Domain: desmoglein repeat <DG4>
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/Domain: extracellular #status predicted <EXT
/Domain: cadherin repeat homology <CR1>
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NID:g162966; PIDN:AAA62709.1; PID:g552318
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Pred. No. 0.
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'AQPPSAT' <KO3>

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N;Alternate names: desmocullin control (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1993 *text_change 22-Jun-1999
C;Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 22-Jun-1999
C;Daccession: A43838; B43838; A38456; A60714; S14542
C;Accession: A43838; B43838; A38456; A60714; S14542
C;Accession: A43838; B43838; A38456; A60714; S14542
R;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Schmelz, M.;
Nifferentiation 47, 29-36, 1991
Nifferentiation 47, 29-36, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Neural crest cell-cell adhesion controlled A;Reference number: I50178; MUID:95309115 A;Accession: I50180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Accession: I50180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
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C;Date: 21-Feb-1997 #sequence_revi
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A; Residues: 1-785 < NAK>
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A; Note: this sequence has been
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Best Local S
Matches 8
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Best Local
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8; Conserv
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9; Conser
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lte: carbohydrate (Asn) (covalent) #status predicte
sequence of bovine muzzle epithelial A43838; MUID:92008912
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Pred. No.
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                                                                   Zimbelmann, R.; Schmelz, M.; Franke,
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F;584,588,678/Binding site: phosphate (Thr) (covalent) (by protein ki F;605/Binding site: phosphate (Ser) (covalent) (by casein kinase II) F;671/Binding site: phosphate (Ser) (covalent) (by protein kinase C) F;681/Binding site: phosphate (Tyr) (covalent) #status predicted F;682/Binding site: phosphate (Thr) (covalent) (by casein kinase II)
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    A;Cross-references: GB:X56966; NID:g315; PIDN:CAA40286.1; R;Mechanic, S.; Raynox, K.; Hill, J.E.; Cownin, P. Proc. Natl. Acad. Sci. U.S.A. 88, 4476-4480, 1991 A;Title: Desmocollins form a distinct subset of the cadher
                                                                                                                                                                                                                                 A; Title: Cloning and A; Reference number: 1 A; Recession: B38456
                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: desmosomal glycoprotein 3
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: B38456; A39377; S14567
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F;223-343/Domain: cadherin repeat homology <CR3>
F;223-338/Domain: cadherin repeat homology <CR3>
F;339-444/Domain: cadherin repeat homology <CR4>
F;445-561/Domain: cadherin repeat homology <CR5>
F;562-582/Domain: transmembrane #status predicted <TMM>
F;562-582/Domain: htracellular #status predicted <INT>
F;31,266,413/Binding site: carbohydrate (Asn) (covalent)
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J. Cell Sci. 97, 239-246, 1990
A;Title: Desmosomal glycoproteins 2 and 3
A;Reference number: A60714; MUID:91115997
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A; Residues: 1-32; 65-76; 148-159; 164-176; 190-205; 208-219; 238-256; 361-375; 377-388; 478-48
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A; Residues: 1-6,'A',8-9,'R',11-17,'RCE',21-23 <HOL>
A; Experimental source: nasal epidermis
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1; Nobecule type: mRNA
1; Nobecule type: mRNA
1; Residues: 606-761 <COL>
A; Residues: 606-761 <COL>
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
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A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g311
A; Cross-references: EMBL: X56967; NID: g310; PIDN: CAA40287.1; PID: g310; PID: g310; PIDN: GAA40287.1; PID: g310; PIDN: GAA40287.1; PID: g310; PID: g310; PIDN: GAA40287.1; PID: g310; PIDN: GAA40287.1; PID: g310; PIDN: GAA40287.1; PID: g311
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                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-839 <COL>
                                                                                                                                                                                                                                                                                                                                              R;Collins, J.E.; Legan, P.K.
J. Cell Biol. 113, 381-391,
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/Domain: cadherin repeat homology <CR1>
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rds: alternative splicing; calcium binding
/Product: desmocollin la #status experimen
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                                                                                                                                                                                                                                                                      sequence analysis of A38456; MUID:91185414
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                                                                                                                                                                                                                                                                                                                                                                                       Kenny, T.P.; MacGarvie, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB pred. No. 8.9; 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.9;
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cadherin family of cell adhesion
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RESULT 9
A48910
desmocollin
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A;Map position: 18q12.2-18q12.2
C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: alternative splicing; calcium binding; cell adhesion; glycoprotein; phosphop
F;67-172/Domain: cadherin repeat homology <CR1>
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A; Residues: 1-484,'A',486-839 <MEC>
A; Cross-references: GB:M67489; GB:M61750; NID:g162970; PIDN:AAA30492.1; PID:g162971
A; Note: part of this sequence, including the amino end of the mature protein, was concidentics:
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C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 15-Aug-1997
C;Accession: B48910
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Best Local Similarity
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A;Molecule type: mR
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
Residues: 1-770 <KIN>
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33-682/Domain: extracellular #status predicted <EXT>
53-62/Domain: cadherin repeat homology <CRL>
55-240/Domain: cadherin repeat homology <CR2>
55-470/Domain: cadherin repeat homology <CR2>
55-470/Domain: cadherin repeat homology <CR3>
71-582/Domain: cadherin repeat homology <CR3>
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Pred. No.
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9.9;
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C/Species: Homo sapiens (man)
C/Date: 12-Aug-1996 #sequence_revision 12-Aug-1996
C/Accession: I37281
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A;Map position: 18q12.2-18q12.2
C;Superfamily: cadherin, cadherin repeat homology
C;Keywords: alternative splicing; calcium binding;
F;67-172/Domain: cadherin repeat homology <CR1>
                                                    C;Accession: I37282
R;Thels, D.G.; Koch, P.J.; Franke, W.W.
Int. J. Dev. Biol. 37, 101-110, 1993
A;Title: Differential synthesis of type 1
A;Reference number: I37281; MUID:93283249
A;Accession: I37282
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C; Date: 08-Dec-1995 #sequence
C; Accession: A48910
                A; Status: preliminary; translated A; Molecule type: mRNA-
                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision
C;Accession: 137282
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A;Residues: 1-840 <RES>
A;Cross-references: EMBL:234522; NID:9505536; PIDN:CAA84278.1; PID:9505537
C;Superfamily: cadherin; cadherin repeat homology
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A;Title: Cloning of the cDNA (DSC1) coding for human type 1
A;Reference number: A48910; MUID:94116981
A;Accession: A48910
                                                                                                                                                                                                              Dsc1b precursor - human
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A; Residues: 1-824 <KIN>
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  A; Residues:
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                              182 FNLFYIEKDTGDI
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7; Conservative
·894 <RES>
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                                    from GB/EMBL/DDBJ
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Pred. No. 9.7;
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EMBL: 234522; NID: g505536; PIDN: CAA84279.1; PID: g505538

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A:Introns: 829/2
C:Superfamily: cadherin; cadherin repeat homology
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Cancer Res. 55, 2206-2211, 1995
A;Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for A;Reference number: 137016; MUID:95262134
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Cancer Res. 54, 3034-3041, 1993
Cancer Res. 54, 3034-3041, 1993
A;Title: Isolation of complementary DNA encoding K-cadherin, A;Reference number: I52701; MUID:94243827
A;Accession: I52701
                                                                                                                                                                                                                                                                                                                                                              K-cadherin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999
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C:Superfamily:
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A; Residues: 1-790 <RES>
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Cross-references: GB:D25290; NID:g435460; PIDN:BAA04975.1;
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RESULT

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C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #second
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C;Species: Gallus gallus (chicken)
C;Date: 21-Feb-1997 #sequence_revision
C;Accession: I50178
                                                                                                                                                                                                                            R;Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, submitted to the EMBL Data Library, May 1996 A;Reference number: H01584
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G02678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:D42149; NID:g867998; PIDN:BAA07720.1; PID:g867999 C;Superfamily: cadherin; cadherin repeat homology
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A;Accession: 150178
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                       A;Cross-references: EMBL:U59325; NID:g1389852; PIDN:AAB02933.1; C;Superfamily: cadherin; cadherin repeat homology
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A; Residues: 1-790 <NAK>
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A;Title: Neural crest cell-cell adhesion
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A; Residues: 1-790 <SHI>
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Title:
Perfect score:
Sequence: OM protein - protein search, using sw model Run on: January 6, 2000, 15:40:34; Search time 51.33 Seconds (without alignments) 6.922 Million cell updates/sec US-08-991-628-3 71 1 LNSKIAFKIVSQEPA 15 GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

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# ALIGNMENTS

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PS Claim 1; Page 39; 58pp; English.

C Chaim 2; Page 39; 58pp; English.

C Chaim 1; Page 39; 58pp; English.

C Chaim 2; Page 39; 58pp; English.

C Chaim 2; Page 39; 58pp; English.

C C All Manar non-collagen or non-myslin basic protein of colorism and individual to an individual to an individual to an individual to an individual to that polypeptide. In both cases, the colorising an individual to that polypeptide. In both cases, the colypeptide (whether self or non-self) includes an amino acid consequence corresponding to a sequence motif for a MHC class II colorism self or non-self) includes an anino acid colorism self or a colorism and colorism and colorism self or a colorism and antoin mune colorism self or non-self) and that human autoimmune colorism in individuals with the autoimmune disease. This peptide is derived from the human desmoglein 3 protein and acids 190-204) and is implicated as a self epitope in pemphigus vulgaris. Peptides of and is implicated as a self epitope in pemphigus vulgaris. Peptides in andividuals with the autoimmune disease.
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Sequence
                          #64813;
29-SEP-1998 (first entry)
Desmoglein-3 190-204.
Desmoglein, DG; gene therapy; pemphigus vulgaris; microparticle;
Desmoglein, DG; gene disease; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from 1
Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strominger JL, Wu WPI: 96-425218/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1996.
07-MAR-1996; U03182.
07-MAR-1995; US-400796.
(HARD) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ното sapiens.
wo9627387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W04843 standard;
W04843;
  Homo sapiens.
US5783567-A.
                                                                                                                                                                         W64815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
influenza; haemagglutinin; reovirus; sigma protein.
                                                                                                                                                                                                 W64815 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8-FEB-1997
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614 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the human desmoglein protein are described in W04841-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wucherpfennig KW
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                                                                                                                                                                                                 peptide;
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Pred. No. le-
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 1;
Pred. No. 1.4e-07
); Mismatches 0
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RESULT
W78814
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PT expression of proteins e.g. in gene therapy
PS Disclosure; Column 4; 42pp; English.
CC The patent describes a new preparation of microparticles each
CC comprising a polymeric matrix and a nucleic acid. The polymeric
CC matrix consists of one or more synthetic polymers having a solubility
CC in water of less than 1 mg/l (e.g. poly-lactic-co-glycolic acid);
CC and at least 90% of the microparticles have a diameter of less than
CC 100 microns. The microparticles are useful for the delivery of nucleic
CC acids to phagocytic cells. In one embodiment the microparticles are
CC less than 20 microns in diameter and the nucleic acid (preferably in
CC closed circular form) includes an expression cortrol sequence
CC coperatively linked to a codding sequence, where the expression product
CC of the coding sequence is a polypeptide having a length and a sequence
CC which permits it to bind to an MHC class I or II molecule. The
CC response in mammals. The present sequence stimulator of an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 15
gene therapy

gene therapy

Disclosure; Page 8; 101pp; English.

A microparticle preparation (MP) has been developed, consisting of microparticles having a diameter of less than 100 mu m. The MP comprises:

(a) a polymeric matrix (PM) consisting of one or more synthetic polymers having a solubility in water of less that 1 mg/l; and (b) an expression vector selected from RNA molecules (at least 50% of which are closed circles) or circular plasmid DNA (at least 50% of which are supercoiled).

Also described is a MP of at most 20 microns in diameter, comprising; (a) a PM; and (b) a NAM comprising an expression control sequence operatively linked to a coding sequence, where the coding sequence encodes an expression product selected from; (1) a polypeptide at least 7 amino expression product selected from; (1) a polypeptide at least 7 amino expression in least 10 and 10 a sequence identical to the sequence of: (1) a fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1998.
22-JAN-1997; US-787547.
22-JAN-1997; US-787547.
(PANG-) PANGAEA PHARM INC.
Curley JM, Hedley ML, Langer R:
WPI; 98-427077/36.
                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1998; U
22-JAN-1998; U
06-JAN-1998; U
22-JAN-1997; U
                                                                                                                                                                                                                                                                                    (PANG-) PANGAEA PHARM INC. Curley JM, Hedley ML, Langer RS, Lunsford LB; WPI; 98-427556/36 New preparations of microparticles - comprising a matrix and nucleic acid comprising an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response in mammals. The present sequence, an antigenic portion of desmoglein 3, is an example of an MHC class II peptide which can be expressed by the nucleic acid. It is associated with pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen; class II associated peptide; pathogen; gene therapy; genetic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desmoglein 3 protein fragment 190-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; downregulation;
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US-787547.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response.
                                                                                                                                                                                                                                                                                             comprising a synthetic expression vector for
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RESULT
W13009
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                                                                                                                                                                                                                                                                   remphigus foliaceus antigen-IgG constant region fusion protein - linked through the hinge region used to treat pemphigus foliaceus Claim 1; Page 10-12; 17pp; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region of IgG linked to the extracellular region of pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus. The antigen is especially administered through an adsorbent upon which the fusion protein is immunodiagnosis. The fusion protein has little or no side effects.
                                                                                                                                                                               Query Match
Best Local S
Matches 12
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25-MAR-1997.
12-SEP-1995;
12-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a naturally-occurring protein from an infectious agent which infects a mammal; (2) a peptide having a length and sequence which permits it to bind to an MHC class I or II molecule; and (3) the polypeptide or the peptide linked to a trafficking sequence. W69763 to W69765, and W78793 to W78897 are peptide fragments for use in the present invention. The MPS are highly effective vehicles for the delivery of polynucleotides into phagocytic cells. They can be used for gene therapy, e.g. for treating genetic diseases, infections or tumours or for downregulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1997 (first entry)

Pemphigus foliaceus antigen-IgG constant region fusion protein.

Pemphigus foliaceus; antoantibody; constant region; IgG;

extracellular region; antigen; hinge portion; skin;

dermatitis herpetiformis; fusion protein; detection; ss.
W13009 standard; protein; 560 AA. W13009; W13009; W1797 (first entry) Segment of desmosomal cadherin, desmoglein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
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                                                                                                                                                                                                                                                        Sequence
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WPI; 97-241758/22.
                                                                                                                                                                                                                                                         in immunodiagnosis.
Sequence 778 AA;
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                                                                                                                      LNSKIAFKIIRQEPS
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                                                                                                                                                                               l similarity 80.
12; Conservative
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JP-260899
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                                                                                                                                                                                               87.3%;
                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Pemphigus foliaceus antigen protein'
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Pred. No.
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Pred. No.
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1.4e-07;
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23-AUG-1995; DE-031033.

24 (PROG-) PROGEN BIOTECHNIK GMBH.

25 Franke WW, Schaefer S;

26 Franke WW, Schaefer S;

27 Franke WW, Schaefer S;

28 WPI; 97-146518/14.

29 Franke WW, Schaefer S;

20 Franke WW, Schaefer S;

20 Franke WW, Schaefer S;

21 Franke WW, Schaefer S;

22 Franke WW, Schaefer S;

23 Franke WW, Schaefer S;

24 Franke WW, Schaefer S;

25 Franke WW, Schaefer S;

26 Franke WW, Schaefer S;

27 Franke WW, Schaefer S;

28 Franke WW, Schaefer S;

29 Franke WW, Schaefer S;

20 Franke WW, Schaefer S;

20 Franke WW, Schaefer S;

20 Franke WW, Schaefer S;

21 Franke WW, Schaefer S;

22 Franke WW, Schaefer S;

23 Franke WW, Schaefer S;

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Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial;
Carcinoma; desmosome; antibody; epitope; diagnosis; detection;
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Purified human E-cadharin protein and nucleic acid - used to develop prods. for diagnosis, prognosis, therapy and prophylaxis of t-cadherin disorders, e.g. malignancies

Claim 1: Page 59-63; 97pp; English.

E-cadherin is a cell adhesion molecule that is also known as conditional cell cam 120/80. The DNA encoding hEC was obtd. by screening normal human liver and hepatocellular carcinoma cDNA libraries and a colonic epithelial cell cDNA library. The following sequences are specifically claimed: AAs 1-878; 151-878; 30 colonic epithelial cell cDNA interacy. The following sequences are specifically claimed: AAs 1-878; 151-878; 30 colonic epithelial cell cDNA interacy. The following sequences are specifically claimed: AAs 1-878; 151-878; 30 colonic epithelial cell cDNA interacy. The following sequences are specifically claimed: AAs 1-878; 151-878; 30 colonic epithelial cell cDNA interacy. The following sequences are specifically claimed: AAs 1-878; 151-878; 30 colonic expression. Suncleotide sequences comprising nucleotide numbers 116-2749; 566-2749; 1-1053; 510-2696; 1332-3000; 540-1500; 348-906; 890-1648; 384-1208; 641-2046; 685-1336; 880-1661; 1199-1742; 1373-1742; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744; 170-1744
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16-NOV-1993; U11097.
17-NOV-1992; US-978897.
(UYYA) UNIV YALE.
MOTION JS, Rimm DL;
WPI; 94-183426/22.
                                                                                                                                                                            Human E-cadherin precursor.
E-cadherin; T-lymphocyte; alpha-E,beta-7 integrin; cell adhesion; autoimmune disease; Crohn disease; psoriasis.
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Sequence
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Sequence of human liver E-cadherin,
Human epithelial-cadherin; E-cadherin;
                                                                                                                                                         Homo sapiens.
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/label= Sig_peptide
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73.3%;
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Pred. No.
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0.0046;
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Matches 7
                                                                                                                  13-JUN-1996.

13-DEC-1995;

09-DEC-1994;

09-DEC-1995;

31-JAN-1995;

05-MAY-1995;

(RPMS-) RPMS:

(RPMS-) RPMS:
wpI; 96-287194/29.

Identifying virulence genes in microorganisms - by introducing mutants with insertion inactivated genes into environment and retrieval and analysis of mutants (laim 51; Figure-41; 131pp; English.

A method for identifying a microorganism having a reduced adaptation to a particular environment comprising the steps of: (1) providing a plurality of microorganisms each of which is independently mutated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure: Page 70-75; 103pp; English.

Disclosure: Page 70-75; 103pp; English.

The human E-cadherin protein precursor (R85487) is expressed by an cDNA clone (T05764) derived from human liver. The extracellular domain of E-cadherin is used to generate peptides that specifically bind to heterotypic cognates of E-cadherin and which inhibit adhesion of intra-epithelial T-lymphoty to E-cadherin-expressing epithelial or endothelial cells in vitro or in vivo, thereby modulating mucosal immune responses. Such peptides are also specifically reactive with a monoclonal antibody (E4.6 or E6.1) that binds to E-cadherin and that can inhibit T-cell binding.
                                                                                                                                                                                                                                                                                                        Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                 Virulence gene cluster polypeptide product. Mutant; adaptation; virulence factor; ident
                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS Brenner MB, Cepek KL; WPI; 95-392921/50.
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                                                                                                                                                                                                                     W09617951-A2
                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                             R97246 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting adhesion isolating agents to psoriasis, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAAIAYTILSQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 53.17; Conservative
                                                                                                                                                                                                                                                                                                                     drugs; infection; treatment.
                                                                                                                               ; G02875.
; GB-024921.
; GB-001881.
; GB-009239.
S TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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US-237919
                                                                                                                                                                                                                     Region /note= "All x's in this sequence correspond termination codons in the virulence gene cluster sequence given in T09224."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Extracellular_uome_n.
/note= "the extracellular domain (amino acids
/note mature protein) is the preferred
region for generation of peptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention 703. .726
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Protein; 4472 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of T lymphocytes with E-cadherin - useful for treat auto-immune diseases e.g. Crohn's disea
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                                                                                                                                                                                                                                                                                                                                    identification;
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19-SEP-1997; U16718.
27-SEP-1996; US-026823.
27-SEP-1996; US-026823.
(AMCY ) AMERICAN CYANAMID CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
MUTPHY BR. Randolph VB, Sidhu MS, Tatem JM
WPI; 98-230710/20.
N-PSDB; V18272.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a unique marker sequence so that each microorganism; (2) providing marker sequence, or clones of the said microorganism; (2) providing individually a stored sample of each mutant produced by step (1) and providing individually stored nucleic acid comprising the unique marker sequence from each individual mutant; (3) introducing a plurality of mutants produced by step (1) into the said particular environment and allowing those microorganisms which are able to do senvironment and allowing those microorganisms which are able to do senvironment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2873
                                                                                                                                                                                                                                                                                                                                               Recombinantly generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus places page 246-254; 426pp; English.

This sequence represents the wild-type L protein from Human parainfluenza virus (HPIV-3) type 3 isolate JS. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' genomic promoter region and at least 1 attenuating mutation in the RNA polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a unique marker sequence so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W48711 standard; Protein; W48711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPIV-3 JS isolate wild-type L protein.
L protein; attenuation; non-segmented; negative sense; vaccine; immunity; single stranded RNA virus; Mononegavirales.
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58.3%;
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      PT Recombinantly generated, attenuated, non-segmented, negative-sense, pri single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus pri polymerase gene, useful as vaccine to immunise against such virus PT polymerase gene, useful as vaccine to immunise against such virus PT polymerase gene, the Human parainfluenza virus (HPIV-3) type 3 cracine FRhl cp45 L protein. This sequence is used in a method which converted the protein region and the virus of the order converge region and at least 1 attenuating mutation in the 3' genomic promoter region and at least 1 attenuating mutation in the RNA colymerase gene, This RNA virus can be used as a vaccine to immunise an conjunctional against such a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                         27-SEP-1996; US-026823.
(AMCY) AMERICAN CYANAMID CO
(USSH) US DEPT HEALTH & HU
MUXPHY BR, Randolph VB, Sid
WPI; 98-230710/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W48712
W48712;
Recombinantly generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus plsclosure; Page 283-291, 425pp; English.

This sequence represents the Human parainfluenza virus (HPIV-3) type 3 vaccine vero cp45 L protein. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' genomic promoter region and at least 1 attenuating mutation in the RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMCY ) AMERICAN CYANAMID CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Murphy BR, Randolph VB, Sidhu MS, Tatem
WPI, 98-230710/20.
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27-SEP-1996; US-026823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human parainfluenza
WO9813501-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-1998 (first entry)
HPIV-3 Vero cp45 vaccine L protein.
L protein: attenuation; non-segmented; negative sense; vaccine; immunity;
single stranded RNA virus; Mononegavirales.
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                                                                                                                                                                                                                                                                                                                                N-PSDB; V18274.
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WO9813501-A2.
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, Sidhu MS, Tatem JM,
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non-segmented; negative sense; vaccine;
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Pred. No. 6.1e
6; Mismatches
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W82841
Search completed: January
Job time: 1683 sec
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                                                                                                                                                                                                       F 19-MAR-1997; 065716.

R 19-MAR-1997; JF-065716.

A (TAIS) 7 TAISHO PHARM CO LTD.

R WPI; 98-575902/49.

R N-PSDB; V64162.

T HUCEP-1 protein having neuron function activating activity - useful for treating ischaemic brain diseases and nerve denaturation conditions such as Parkinson's and Alzheimer's diseases.

C Claim 1; Fig 4; 17pp; Japanese.

C The present sequence represents human cerebral protein-1 (HUCEP-1).

C HUCEP-1 has neuron function activating activity. HUCEP-1 is useful conditions such as Parkinson's and Alzheimer's diseases.

C Sequence 456 AA;
                                                                                                                               Query Match 47.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 47.9
Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.

Sequence 2233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
J10257891-A.
29-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cerebral protein-1; HUCEP-1; ischaemic brain disease; neuron function activating activity; nerve denatured disease; Parkinson's disease; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W82841 standard; Protein; 456 AA. W82841;
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973 LDRSVLYRIMNQEP 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uman cerebral protein-1
                                                                         408 TKLGFKIVSKD 418
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                 6, 2000, 15:40:36
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Pred. No. 6.1e+02;
6; Mismatches 3; Indels
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Perfect score:
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10.858 Million cell updates
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cadherin - African
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virR49 protein – s
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Ksp-cadherin - rab
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Autoantibodies against a novel epithelial cadherin in pemphigus vulgaris, a
A;Reference number: A41088; MUID:92069753
A;Accession: A41088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      desmoglein 3 precursor - human
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A; Residues: 1-999 < AMA>
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S63634	ZLNZSE	ZLNZSV	S24382	CFRZ	CFNT	CFPM	B75009	S64146	н64386
ribosomal protein	genome polyprotein	genome polyprotein	nitrous-oxide redu	plastoqu <b>inolplas</b>	plastoquinoiplas	plastoquinolplas	ribonucleotide red	probable mem <b>brane</b>	hypothetical prote

### ALIGNMENTS

Klaus-Kovtun, V.; Stanley, J.R.

GB:M76482; NID:g190751; PIDN:AAA60230.1; PID:g190752

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submitted to the EMBL Data Library, November 1990 A; Reference number: $16906 A; Accession: $16906 A; Accession: $16906 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: S16906; A39706; A61254; A61279; S16158
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A;Map position: 18q12.1-18q12.2
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Matches 15
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desmoglein repeat <DG2>
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Pred. No. 2.6e-05;
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IJBO21
desmoglein 1 precursor - bovine
N;Alternate names: desmoglein BDGM
C;Species: Bos prinigenius taurus (cattle)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 2;
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 2;
C;Accession: $14603; A38872; A37785; S38721; A48173; S24412
R;Koch, P.J.; Goldschmidt, M.D.; Zimbelmann, R.; Franke, W.W.
submitted to the EMBL Data Library, March 1991
submitted to the EMBL Data Library, March 1991
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A;Cross-references: EMBL:X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
A;Cross-references: EMBL:X56654; NID:g30505; PIDN:CAA39976.1; PID:g30506
R;Wheeler, G.N.; Parker, A.E.; Thomas, C.L.; Atallotis, P.; Poynter, D.; Arnemann, J.; Proc. Natl. Acad. Sci. U.S.A. 88, 4796-4800, 1991
A;Title: Desmosomal glycoprotein DGI, a component of intercellular desmosome junctions, A;Reference number: A39706; MUID:91271279
A;Accession: A39706
A; Accession: S14603
A; Molecule type: mRNA
A; Residues: 1-1043 < KOC>
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A;Title: Desmosomal glycoproteins I, II and III: novel A;Reference number: A61279; MUID:92175187
A;Accession: A61279
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A; Residues: 1-55 <WH3>
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A;Title: Structural analysis and expression of human desmoglein: & A;Reference number: A61254; MUID:92121251
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A; Residues: 24-1049 <
                                                                                   A; Reference number: S14603
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Best Local S
Matches 12
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:Superfamily: cadherin; cadherin repeat homology
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Cross-references: GB:X56654
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928-956/Domain: desmoglein repeat <DG4>
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160-269/Domain: cadherin repeat homology <CR2>
272-385/Domain: cadherin repeat homology <CR3>
392-493/Domain: cadherin repeat homology <CR4>
509-530/Region: serine/threonine-rich
549-569/Domain: taransmembrane *status predicted <
572-1049/Domain: intraceilular *status predicted
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; Pred. No. 0.00
2; Mismatches
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0.0014;
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A;Cross references: EMBL:X58466; NID:g306; PIDN:CAA41380.1; R;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R. Eur. J. Cell Biol. 55, 200-208, 1991
A;Title: Complete amino acid sequence of the epidermal desmc A;Reference number: A38872; MUID:92037656
A;Accession: A38872.
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R;Goodwin, L.; Hill, J.E.; Raynor, K.; Raszi, L.; Manabe, Biochem. Biophys. Res. Commun. 173, 1224-1230, 1990
A;Title: Desmoglein shows extensive homology to the cadhes A;Reference number: A37785; MUID:91097553
A;Accession: A37785
C:Species: Homo sapiems (man)
C:Date: 20-Feb-1995 *sequence_revision
C:Accession: S38673; B38872
                                                                                                                                               RESULT
S38673
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A;Residues: 44-123,'V',125-493 <GOO>
A;Cross-references: GB:M38165; NID:9162966; PIDN:AAA62709.1; PID:9552318
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A; Residues: 1-87; 968-1043 < KO2>
                                                                                       desmoglein 2 - human
N;Alternate names: desmoglein HDGC
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A;Cross-references: GB:X57784
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(876-905/Domain: desmoglein repeat cDG2>
906-933/Domain: desmoglein repeat cDG3>
934-962/Domain: desmoglein repeat cDG4>
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Best Local
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52-157/Domain: cadherin repeat homology <CR1>
160-269/Domain: cadherin repeat homology <CR2>
272-385/Domain: cadherin repeat homology <CR3>
392-91/Domain: cadherin repeat homology <CR3>
392-91/Domain: cadherin repeat homology <CR4>
549-574/Domain: transmembrane #status predicted <TMM>
549-574/Domain: intracellular #status predicted <INT>
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4-49/Domain: propeptide #status predicted <PRO>
0-1043/Product: desmoglein #status predicted <PRO>
0-549/Domain: avtracallular forms.
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12; Conser
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Pred. No. 0.0014;
2; Mismatches
                                20-Feb-1995 #text_change 20-Aug-1999
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submitted to the EMBL Data Library, September 1993 A;Reference number: S38673 A;Accession: S38673
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A;Map position: 18q12.1-18q12.2
C;Superfamily: cadherin; cadherin repeat homology
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A;Cross-references: EMBL:Z.26317; NID:g416177; PIDN:CAA81226.1; PID:g416178
A;Cross-references: EMBL:Z.26317; NID:g416177; PIDN:CAA81226.1; PID:g416178
A;Cross-reference, EMBL:Z.26317; NID:g416177; Zimbelmann, R.; Franke, W.W.
Experimental Composition of the Experimental Mesmoglein precursor polypeptide
A;Title: Complete amino acid sequence of the epidermal desmoglein precursor polypeptide
A;Reference 'number: A38872; MUID:92037856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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A; Residues: 777-1117 <KOC>
                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 157-884 <RIN>
A; Cross-references: EMBL: X06339
A; Cross-references: EMBL: X06339
A; Note: part of this sequence, including the amino end of the mature R; Behrens; J.; Loewrick, O.; Klein-Hitpass, L.; Birchmeier, W. Proc. Natl. Acad. Sci. U.S.A. 88, 11495-11499, 1991
A; Title: The E-cadherin promoter: Functional analysis of a G-C-rich r A; Reference number: 149565; MUID: 92107977
A; Accession: 149565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 22-Jun-1999
C;Accession: S04528; S03160; I49565; S48735
R;Nagafuchi, A.; Shirayoshi, Y.; Okazaki, K.; Yasuda, K.; Takeichi, M.
Nature 329, 341-343, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-cadherin | N; Alternate
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                       FEBS Lett. 352, 318-322, 1994
A;Title: Purification and spectroscopic characterization A;Reference number: S48735; MUID:95010732
A;Accession: S48735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: S03160
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                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-15 <RES>
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;Residues: 1-412,'V',414-884 <NAG>
;Cross-references: EMBL:X06115
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                                                                                                                                       references: GB:M81449; NID:g192325; K.I.; Yau, P.; Overduin, M.; Bagby,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNSKISYRIVSLEPA 205
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ll; Conservative
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Pred. No.
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                                                                                                                                          PIDN:AAA37352.1; PID:g192326
S.; Porumb, T.; Takeichi, M.;
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IJCHCH
B-cadherin precursor - chicken (1149,000).
N;Alternate names: K-CAM protein
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1993 #text_change
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
C;Accession: A41634; -A89715; S16160
C;Accession: A41634; -A89715; S16160
R;Sorkin, B.C.; Gallin, W.J.; Edelman, G.M.; Cunningham, B.A.
R;Sorkin, B.C.; Gallin, W.J.; Edelman, G.M.; Cunningham, B.A.
R;Sorkin, B.C.; Gallin, W.J.; Edelman, G.M.; Cunningham, B.A.
R;Sorkin, B.C.; Gallin, W.J.; Edelman, G.M.; Cunningham, B.A.
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RESULT IJCHCB

molecules

have

similar

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A; Molecule type: protein
A; Residues: 156-300 <TON>
C; Comment: Cadherins mediate
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                                                                                                                                                                                                                              A; Reference number: S34438; MUID:92093614
A; Accession: S34438
A; Status: preliminary; nucleic acid sequence
A; Molecule type: DNA
A; Residues: 1-884 <RIN>
A; Cross-references: EMBL:X60975
                                                                                                                                                                                                                                                                                                              R;Ringwald, M.; Baribault, H.; Schmidt, C.;
Nucleic Acids Res. 19, 6533-6539, 1991
A;Title: The structure of the gene coding fo
A;Reference number: S34438; MUID:92093614
                                                                                                                                                                                                                                                                                                                                                                  uvomorulin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision
C;Accession: S34438
R;Ringwald, M.; Baribault, H.; Schmidt,
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489-597/Domain:
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Best Local
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8; Conservative
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n: cadherin binding #status predicted
n: cadherin repeat homology <CR2>
n: cadherin repeat homology <CR3>
n: cadherin repeat homology <CR3>
n: cadherin repeat homology <CR4>
n: cadherin repeat homology <CR4>
n: cadherin repeat homology <CR4>
n: transmembrane #status predicted <TMM
n: intracellular #status predicted <INT
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A:Gene: fat
A:Gene: fat
A:Gene: fat
A:Gross-references: FlyBase:FBgn0001075
A:Gross-references: FlyBase:FBgn0001075
C:Superfamily: cadherin-related tumor suppressor; cadherin repeat homology;
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane prote
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane prote
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane prote
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protection and calcium binding; duplication;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 16-Feb-1997 C;Accession: A41087; B41087 B41087 B;Accession: A41087; B41087 B;Accession: A41087; B41087 B;Accession: A41087; Meber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, C.S. cell 67, 853-868, 1991 A;Biessmann, Biessmann, H.; Bryant, P.J.; Goodman, C.S. cell 67, 853-868, 1991 A;Accession: A41087; MUID:92069752 A;Accession: A41087; MUID:92069752
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A; Residues: 143-485;1279-5147
A; Cross-references: GB:M80537
A; Accession: B41087
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A;Residues: 7-413,'V', 415-732 <NAP>
A;Cross-references: GB:X58518; NID:963113; PIDN:CAA41408.1; E
C;Comment: Cadherins mediate calcium-dependent intercellular
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A;Cross-references: GB:M81894; NID:g212226; PIDN:AAA48929.1; PID:g212227
A;Cross-references: GB:M81894; NID:g212226; PIDN:AAA48929.1; PID:g212227
R:Napolitano, E.W.; Venstrom, K.; Wheeler, E.F.; Reichardt, L.F.
J. Cell Biol. 113, 893-905, 1991
J. Cell Biol. 113, 893-905, 1991
A;Title: Molecular cloning and characterization of B-cadherin, a novel chick cadherin.
A:Reference number: A38715; MUID:91225083
A;Accession: A38715
                                                                               F:36-5147/Product: cadherin-related tumor suppressor #status F:36-4583/Domain: extracellular #status predicted <EXT> F:51-156/Domain: cadherin repeat homology <CRI>
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A; Residues: 1-42; 487-1278 <MA2>
A; Cross-references: GB: M80537
A; Note: 1229-Gly and 1233-Ser were also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;448-552/Domain: 0
7;555-580/Domain: 1
7;581-732/Domain: 1
7;689-702/Region: 2
7;137,410/Binding:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Ma
Best Loc
Matches
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84-89/Region: cadherin binding #status predicted;
117-227/Domain: cadherin repeat homology <CR2>
;230-339/Domain: cadherin repeat homology <CR3>
340-447/Domain: cadherin repeat homology <CR4>
;448-552/Domain: cadherin repeat homology <CR5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Introns: 29/3; 81/3; 130/1; 188/3; 231/3; 293/3; 375/2; 423/1; 498/1; 571/1; 614/3; 66; superfamily: cadharin; cadharin repeat homology; superfamily: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro; 1-6/Domain: propeptide (fragment) #status predicted <PRO>; 1-65/Domain: extracellular #status predicted <EXT>; 7-732/Product: B-cadherin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
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Local
30/Domain: cadherin repeat homology <CR2>
270/Domain: cadherin repeat homology <CR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NSKIAFKIVSQEP
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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site: carbo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1 Pred. No. 8.9; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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r adhesion,
                                                                                                                                                                                 predicted <MAT>
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F;602-708/Domain: cadherin repeat homology <CR4>
F;718-822/Domain: cadherin repeat homology <CR5>
F;718-822/Domain: cadherin repeat homology <CR7>
F;831-942/Domain: cadherin repeat homology <CR8>
F;948-1049/Domain: cadherin repeat homology <CR9>
F;948-103/Domain: cadherin repeat homology <CR9>
F;1052-1113/Domain: cadherin repeat homology <CR9>
F;1156-1178/Domain: cadherin repeat homology <C11>
F;1156-1178/Domain: cadherin repeat homology <C12>
F;1387-1489/Domain: cadherin repeat homology <C12>
F;1387-161/Domain: cadherin repeat homology <C12>
F;1492-1601/Domain: cadherin repeat homology <C15>
F;1492-161/Domain: cadherin repeat homology <C15>
F;171-1823/Domain: cadherin repeat homology <C16>
F;1826-1922/Domain: cadherin repeat homology <C17>
F;1925-2027/Domain: cadherin repeat homology <C19>
F;2028-2167/Domain: cadherin repeat homology <C19>
F;2028-218/Domain: cadherin repeat homology <C29>
F;2287-2491/Domain: cadherin repeat homology <C29>
F;2287-2491/Domain: cadherin repeat homology <C29>
F;2192-2703/Domain: cadherin repeat homology <C29>
F;2193-2313/Domain: cadherin repeat homology <C29>
F;2192-2703/Domain: c
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R;Rounsley, S.D.; Lin, X.; K
submitted to the EMBL Data L
A;Description: Arabidopsis t
A;Reference number: Z14676
A;Accession: T02501
A; Intron
A; Note:
                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1421 <ROUD
A;Residues: 1-1421 <ROUD
A;Cross-references: EMBL:AC004683; NID:g3395421; PID:g3395428
A;Experimental source: cultivar Columbia
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                               A; Map position:
A; Introns: 52/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T19C21.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 14-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;4096-4127/Domain:
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Best Local S
Matches 7
                                                                                              Genetics:
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   T19C21.7
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                                                                  N
                            107/1; 148/2; 191/3; 212/2; 1317/3; 1346/3
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cadherin repeat home
EGF homology <EG1>
EGF homology <EG2>
EGF homology <EG3>
EGF homology <EG4>
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Library,
thaliana
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                            K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, August 1998
                                                                                                                                                                                                                                                                                                                                                                             chromosome II BAC T19C21 genomic sequence
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Query Match Best Local S Matches 6

Similarity 42. 6; Conservative

56.3%; 42.9%;

Score 40; DB Pred. No. 29; 7; Mismatches

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Length 1421; l; Indels

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Gaps

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Nucleic Acids Res. 18, 5896, 1990
A;Title: Human N-cadherin: nucleo
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                                                                                                                                                           8
                                                             RESULT
                   cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA;
Residues: 160-194,'IR',197-211,'L',213-227,'Q',229,'N',231-235,'G',237-248,'T',250-356;
Cross-references: GB:M34064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: S11487; MUID:91016946
Accession: S11487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: flomo sapiens (man)
Date: 30-Jun-1993 #sequence_revision 30-Jun-1993;
Accession: A38870; S11487; JQ0751; S13799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title: N-cadherin gene maps to human chromosome 18 and is not linked to the E-cadherin Reference number: JQ0751; MUID:90347462 Accession: JQ0751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA
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                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keywords: calcium binding; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: cadherin; cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:128185; OMIM:114020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comment: Cadherins mediate calcium-dependent intercellular
                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ross-references: EMBL:X54315; NID:g34998; PIDN:CAA38213.1; PID:g34999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ssidues: Ī-340,'N',342-698,'R',700-704,'F',706-906 <RE2>:oss-references: EMBL:X54315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te: this sequence has been revised in reference A38870 lsh, F.S.; Barton, C.H.; Putt, W.; Moore, S.E.; Kelsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 VDSKISYEIITQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position:
                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LNSKIAFKIVSQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:CDH2; NCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 precursor - human
                                                                                                                                                             1 LNSKIAFKIVSQEPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain:
                                                                                                                           LNGMLRYRIVSQAPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-906 <REI>
                                                                                                                                                                                                       . Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                     cadherin repeat homology <CR4> cadherin repeat homology <CR5> transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                  cadherin repeat
cadherin repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extracellular #status
                                                                                                                                                                                                                                                                                                                                               transmembrane #status predicted intracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cadherin repeat homology <CRl>
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xr - human
ARC-1; cell CAM 120/80; E-cadherin; epithelial cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275
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                                                                                                                                                                                                                             54.98;
46.78;
                                                                                                                           314
                                                                                                                                                                                                                                                                                                             651,692/Binding site: carbohydrate (Asn) (covalent) #status pr
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                                                                                                                                                                                                         4:
                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deduced amino acid
                                                                                                                                                                                                                                 DB 1;
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        duplication;
                                                                                                                                                                                                                                                                                                                                                                             AMI'V
                                                                                                                                                                                                                                                                                                                                                        <INT>
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                                                                                                                                                                                                            4.
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                                                                                                                                                                                                                                                    Length 906
                                                                                                                                                                                                              Indels
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                           A;Cross-references: GB:L34545; NID:g509604; PIDN:AAA21764.1; PID:g509605 R;Becker, K.F.; Atkinson, M.J.; Reich, U.; Becker, I.; Nekarda, H.; Siew Cancer Res. 54, 3845-3852, 1994
                                                                                           A; Molecule type: DNA
A; Residues: 1-16 < RES>
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L-CAM;

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diffuse type gastric

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R;Kelker, W.; Warda, A.; Oda, T.; nitulesta, V.;
submitted to the EMBL Data Library, December 199;
A;Description: Sequence of human E-cadherin cDNA
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                                                                                                               A;Residues: 1-9'G',11-15,'RSPLGSQERSPPPCLTRELHYHGAPAPPEKRPR',52-67,'I',69,'LTPIP',7:
A;Cross-references: GB:L08599; NID:g340184; PIDN:AAA61259.1; PID:g340185
A;Note: the majority of differences between this and other reports represent apparana, Note: the authors translated the codon CCG for residue 868 as Arg
R;Bussemakers, M.J.G.; GITO181, L.A.; van Bokhoven, A.; Schalken, J.A.
Biochem. Biophys. Res. Commun. 203, 1284-1290, 1994
A;Title: Transcriptional regulation of the human E-cadherin gene in human prostate c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 'XQ',157-162,'V',164-179 <WHED R; Berx, G.; Staes, K.; van Hengel, J.; Molemans, Genomics 26, 281-289, 1995 
A; Title: Cloning and characterization of the humans, A; Reference number: A57171; MUID:95324920
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A; Residues: 265-392 <FRI>
A; Cross-references: EMBL: X52279; NID: g28821;
A; Cross-references: EMBL: X52279; NID: g28821;
R; Wheelock, M.J.; Buck, C.A.; Bechtol, K.B.;
J. Cell. Biochem. 34, 187-202, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-882 <BUS>
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A; Accession: S31460
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                                            A; Accession: I52294
                                                                                    A;Reference number: I52294; MUID:94380041
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
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Title: Characterization and chromosomal locations of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the comp
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Accession: S05475
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Note: nucleotide sequence is not
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Residues: 1-542,'F',
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Residues: 157-311 <MAN>
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ference number: S31460
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translation not shown; translated from GB/EMBL/DDB
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128, 1993
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(1rohash1, S.; Kemler, R.; Birchmeier,
December 1992
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Kemler, R.
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Damsky, C.H.
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R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: S73327; MUID:97105885
A;Accession: S73915
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                                                                                                                                                                                                                          A; Genetic code: SGC3
C; Superfamily: virulence-associated protein vacB homolog
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A; Residues: 1-726 <HIM>
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N:Alternate names: hypothetical protein K04_orf726
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;Residues: 337-476 <RE2>
;Residues: 337-476 <RE2>
;Cross-references: GB:$72492; NID:g632756
                                                                                                                                             Query Match
Best Local
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mes 7; Conserv
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calcium binding; cell adhesion; dupli
                                                                                                                          Similarity 50.07; Conservative
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22.1-16q22.1
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ar #status predicted <EXT>
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Pred. No. 21;
4; Mismatches
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                                                              RESULT
N-cadherin 1 precursor African clawed C; Species: Xenopus laevis (African clawed C; Date: 30-Jun-1993 #sequence_revision:
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RESULT

can clawed frog rican clawed frog) \_revision 30-Jun-1993

#text\_change 19-Jan-1996

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J. Biol. Chem. 270, 17594-17601, 1995
A;Title: Isolation and cDNA cloning of Ksp-cadherin, a A;Reference number: I46536; MUID:95340560
A;Saccession: I46536
A;Status.
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A;Accession: A43785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-cadherin
C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-906 <GIN>
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A; Residues: 1-829 <THO>
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                                                                                                                                                                                                                                                                                                                                                                                                                          Comment: Cadherins mediate calcium-dependent interce superfamily: cadherin; cadherin repeat homology (Keywords: calcium binding; cell affector, duplication); E8/Domain: signal sequence #status predicted <SIG>29-160/Domain: propeptide #status predicted <PRO>161-966/Product: N-cadherin 2 #status predicted <MAT
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Best Local
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Best Local Similarity
Matches 8; Conserv
                                                                                  Matches
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63-268/Domain: cadherin repeat homology <CR1>
38-243/Region: cadherin binding #status predicted
71-383/Domain: cadherin repeat homology <CR2>
302 NGMLRYKILSQTPA 315
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                                      NSKIAFKIVSQEPA 15
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Xenopus laevis (African clawed frog)
-----1993 #sequence_revision 30-Jun-1993
                                                                                Similarity 7; Conserv
                                                                                                                                                                            ion: serine-rich
,573,623,652,693/Binding site: carbohydrate (Asn) (covalent) #status
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             9:29-100/Domain: propeptide #status predicted <PRO>
7:161-905/Product: N-cadherin 1 #status predicted <PRO>
7:161-13/Domain: extracellular #status predicted <PRO>
7:163-268/Domain: cadherin repeat homology <CRI>
7:238-243/Region: cadherin binding #status predicted <PRO>
7:213-383/Domain: cadherin repeat homology <CR2>
7:201-383/Domain: cadherin repeat homology <CR2>
7:386-498/Domain: cadherin repeat homology <CR3>
7:501-606/Domain: cadherin repeat homology <CR3>
7:501-606/Domain: cadherin repeat homology <CR4>
7:607-713/Domain: cadherin repeat homology <CR5>
7:14-745/Domain: transmembrane #status predicted <INT>
7:14-905/Domain: transmembrane #status predicted <INT>
8:67-8:77/Region: agrina-10-h
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Best Local Similarity 50.0%;
Matches 7; Conservative
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,573,623,651,692/Binding site: carbohydrate (Asn) (covalent) #status pi
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Pred. No. 42;
3; Mismatches 4; Indels
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Title:
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Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Eutheria; F
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"Autoantibodies against a novel epithelial cadherin
"ulgaris, a disease of cell adhesion.";
Cell 67:869-877(1991).
-I- FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS
FILAMENTS MEDIATING CELL-CELL ADHESION.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSIL,
                                                                                                                                                                                                            CHAIN
DOMAIN
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PIR; A41088; IJHUG3.
HSSP; P09803; 1EDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Homo sapiens (Human).
Motazoa; Chordata;
                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P09803;
MIM; 169615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - DOMAIN: CALCIUM MAY BE BOUND BY
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                                                                                                                                                                                      TRANSMEM
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(POTENTIAL).

(POTENTIAL).

DISEASE: PEMPHIGUS VULGARIS (PV) IS A POTENTIALLY LETHAL SKIN DISEASE IN WHICH EPIDERWAL BLISTERS OCCUR AS THE RESULT OF THE LOSS OF CELL-CELL ADHESION CAUSED BY THE ACTION OF AUTOANTIBODIES AGAINST DSG3.

SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                          PF00028;
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200444
                                                                                                                                                                                                                                                                                                                            PS00232; CADHERIN; 3.
esion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primates;
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(Rel. 27, Last sequence update)
(Rel. 35, Last annotation updat
3 PRECURSOR (130 KD PEMPHIGUS VU
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    Catarrhini;
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TER1_CAEEL
VACB_SHIFL
ASNH_METJA
BEM4_YEAST
YSNK_CAEEL
POTENTIAL.
CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
DESMOGLEIN R
DESMOGLEIN R
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POTENTIAL.
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POTENTIAL.
DESMOGLEIN 3.
EXTRACELLULAR (
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AND INTERMEDIATE
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CARBOHYD
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SEQUENCE
                                                                                                                   "Desmoglein shows extensive homology to the cadherin family of c adhesion molecules.";
Biochem. Biophys. Res. Commun. 173:1224-1230(1990).
-: FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS.
INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDI FILAMENTS MEDIATING CELL-CELL ADHESION.
-!: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!: SUBCELLULAR CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-MUZZLE EPITHELIUM;
KOCH P.J., GOLDSCHMIDT M.D.,
Submitted (MAR-1991) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                           SEQUENCE OF 44-493 FROM N.A. MEDLINE; 91097553.
                                                                                                                                                                                                                                                                                                   "Complete amino acid sequence of the epidermal desmoglein precursor polypeptide and identification of a second type of desmoglein gene. Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (Rel. 27, Created)
01-CCT-1993 (Rel. 27, Last sequence update)
01-CCT-1993 (Rel. 35, Last annotation update)
DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSG1_BOVIN
Q03763;
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                                                                                                                                                                                                                                                                                                                                                                                                                               molecules."
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"Identification of desmoglein, a
glycoprotein, as a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91168965
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                                                                                            SIMILARITY: BELONGS TO THE CADHERIN FAMILY. DESMOSOMAL SUBFAMILY.
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l Similarity 100.0%;
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EMBL/GenBank/DDBJ databases.
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Pred. No. 1.7
0; Mismatches
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1; 4891F6AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                          constitutive desmosomal cadherin family of cell
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1.2e-05;
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AND INTERMEDIATE
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amily of cell
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SG1_HUMAN

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STANDARD;

AC 002413;

AC 002413;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

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PFAM; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X58466; CAA41380.1;
EMBL; X57784; CAA40930.1;
EMBL; M58165; AAA62709.1;
PIR; S14603; IJBOG1.
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                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                               EQUENCE FROM N.A. ISSUE-KERATINOCYTES; EDLINE; 91271279.
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          OC. Natl. Acad. Sci. U.S.A. 88:4796-4800(1991).

FUNCTION: COMPONENT OF INTERCELLULAR DESMOSME JUNCTIONS. FUNCTIONS. PLAQUE PROTEINS AND INTERMEE INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEE FILAMENTS MEDIATING CELL-CELL ADHESION.

SUBCELLULAR-BOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: EPIDERMIS, TONGUE, TONSILAND ESOPHAGUS.

DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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                                                                                                                                                                   a component of intercellular desmosome cadherin family of cell adhesion
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0.00067;
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WATT F.M., RE
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                                                                           TISSUE-COLON CARCINOMA;
TISSUE-COLON CARCINOMA;
MEDLINE; 94192736.
SCHAEFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human ratalogue of the desmoglein s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X56654; CAA39976.1;
PIR; S16906; IJHUG1.
HSSP; P09803; 1EDH.
MIM; 125670; -.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00232; CADHERIN; 2.
Cell adhesion; Signal; Transmembrane; Cytoskeleton; Glycoprotein;
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                                                                     expression catalogue cadherins.";
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SEQUENCE OF 777-1117 MEDLINE; 92037656.
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2 PRECURSOR
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EXTRACELLULAR
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Pred. No. 0.00067;
2; Mismatches 1
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W; FDD79961 CRC32;
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CYTOPLASMIC (POTENTIAL)
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subfamily of
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P09803; Q61377;
P19803; Q61377;
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Cell adhesion; Glycoprotein; Cytoskeleton; Calcium-binding
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HSSP; P15116; INCI.
MIM; 125671; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete amino acid sequence of the epidermal desmoglein preopolypeptide and identification of a second type of desmoglein Eur. J. Cell Biol. 55:200-208(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOCH P.J.,
                                                                       Ol-MAR-1989 (Rel. 10, Greated)
Ol-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1989 (Rel. 36, Last annotation update)
EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (UVOMORULIN) (ARC-1).
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   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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FUNCTION: COMPONENT OF INTERCELLULAR DESMOSOME JUNCTIONS INVOLVED IN THE INTERACTION OF PLAQUE PROTEINS AND INTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: AI
DOMAIN: CALCIUM MAY BE
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SUBCELULIAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
TISSUE SPECIFICITY: ALL OF THE TISSUES TESTED AND CARCINOMAS.
DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
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W; 84D3B898 CRC32;
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                                                                                                                                                                                                                                                                                         OVERDUIN M., TONG K.I., KAY C.M., IKURA M.;

"1H, 15N and 13C resonance assignments and monomeric structure of amino-terminal extracellular domain of epithelial cadherin.";

J. Biomol. NMR 7:173-189(1996).

-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEITHEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 157-260 MEDLINE; 96271285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecule uvomorulin.";
Nucleic Acids Res. 19:6533-6539(1991).
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"The structure of the gene
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Nature 329:341-343(1987).
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MEDLINE; 96176249.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAGAR B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BERRENS J., LOEWRICK O., KLEIN-HITPASS L., BIRCHMEIER W.;
"The E-cadherin promoter: functional analysis of a G.C-rich reg
and an epithelial cell-specific palindromic regulatory element.
Proc. Natl. Acad. Sci. U.S.A. 88:11495-11499(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The structure of cell adhesion molecule uvomorulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ICR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structural basis of calcium-induced
                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: NON-NEURAL EPITHELIAL TISSUES.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecular mechanism of
) J. 6:3647-3653(1987).
                                      X60962;
X60964;
X60965;
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 CAA43292.1;
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CAA43292.1;
CAA43292.1;
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ELZ R., JAEHNIG F., E
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Matches 8
SEQUENCE OF 7-732 FROM N
TISSUE-EMBRYONIC BRAIN;
MEDLINE; 91225083.
NAPOLITANO E.W., VENSTRO
"MOLECULAR CLONITY and c
Cadherin.";
J. Cell Biol. 113:893-90
                                                                                                                                                                                                                                                                                                                                                                                                    CADB_CHICK
P33145;
01-OCT-1993
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CARBOHYD
CONFLICT
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SEQUENCE
                                                                                                                                                          SORKIN B.C., GALLIN W.J., EDELMAN G.M., CUNNINGHAM B.A.; "Genes for two calcium-dependent cell adhesion molecules structures and are arranged in tandem in the chicken gene proc. Natl. Acad. Sci. U.S.A. 88:11545-11549(1991)...
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TRANSMEM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1993 (Rel.
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01-OCT-1993 (Rel.
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Cell adhesion; Glycoprotein; Phosphorylation;
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PFAM; PF01049; Cadherin_C_term;
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X60971; CAA43292
X60972; CAA43292
X60973; CAA43292
X60974; CAA43292
X60975; CAA43292
X60975; CAA43292
X60975; CAA325645
X6039; CAA327352
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972; CAA43292.1
973; CAA43292.1
974; CAA43292.1
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     CADHERINS ARE
                     113:893-905(1991)
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                                                      , REICHARDT
B-cadherin,
     CELL
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     ADHESION PROTEINS
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EMBL; X58518; CAAA1408.1; -.
PIR; A41634; IJCHCB.
HSSP; P09803; ISUH.
PFAM; PF00028; cadherin; 5.
PFAM; PF01049; Cadherin; 1
PROSITE; PS00232; CADHERIN; 3.
Cell adhesion; Glycoprotein; Phos;
SEQUENCE FROM N.A.
MEDLINE; 92069752.
MAHONEY P.A., WEBER U., ONC
GOODMAN C.S.;
"The fat tumor suppressor g
of the cadherin gene superi
                                                                                                       01-FEB-1994 (Rel. 2
01-FEB-1996 (Rel. 3
15-JUL-1998 (Rel. 3
CADHERIN-RELATED TU
                                                                                                              FAT_DROME
P33450;
01-FEB-1994
01-FEB-1996
15-JUL-1998
                                                                    Drosophila
Eukaryota;
Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                            Ephydroidea;
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European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBRYOGENESIS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO SORTING OF HETEROGENEOUS CELL TYPES. B-CADHERIN MAY HAVE IMPORTUNITIONS IN NEUROGENESIS, IN AT LEAST SOME EPITHELIA, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                               Similarity 61.
8; Conservative
                                                            Metazoa; Arthropoda; Tracheata; H
Neoptera; Endopterygota; Diptera;
a; Drosophilidae; Drosophila.
                                                                                     melanogaster
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suppressor gene in gene superfamily."
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                          ONOFRECHUK P.,
                                                                                     (fruit fly)
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annotation update)
PRESSOR PRECURSOR (

    Phosphorylation; Transmembrane;

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CYTOPLASMIC
CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
SER-RICH.
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Pred. No. 4.5;
2; Mismatches
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9C3CF5E9 CRC32;
         Drosophila
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                          BIESSMANN H.,
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                                                                     Hexapoda; Inse
; Brachycera;
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EMBL; M80537; AAA28530.1; PIR; A41087; IJFFTM.
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PROSITE; PS000232; CADHERIN; 22.
PROSITE; PS00022; EGE\_1; 4.
PROSITE; PS01186; EGF\_2; 2.
Cell adhesion; Signal; Transmication—binding. 5147 4583 5147 5147 270 270 382 708 Transmembrane; Cytoskeleton; t; EGF-like domain. CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN-RELATED TUMOR SUE EXTRACELLULAR (POTENTIAL) CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN CADHERIN CYTOPLASMIC CADHERIN POTENTIAL Glycoprotein; SUPPRESSOR

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MEDITINE: 93211394.
BUSSEMAKERS M.J.G., MEES S.G.M., VAN BOKHOV
SCHALKEN J.A.;
"Molecular cloning and characterization of
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01-OCT-1989 (Rel. 12, Created)
01-UTL-1993 (Rel. 26, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (UVOMORULIN) (CAM 120/80).
                            MEDLINE; 94173928.

ODA T., KANAI Y., OYAMA T., YOSHIURA K., SHIMOYAMA Y., SUGIMURA T., HIROHASHI S.;
"E-cadherin gene-mutations in human gastric carcinoma "E-cadherin gene-mutations in human gastric carcinoma proc. Natl. Acad. Sci. U.S.A. 91:1858-1862(1994).
                                                                                                                                                                                                                                               MEDLINE; 95049851.

KANAI Y., ODA T., TSUDA H., OCHIAI A.,

"Point mutation of the E-cadherin gene
of the breast.";
                                                                                                                                                                                                                                                                                                                                                       VARIANTS ALA-370 AND ASN-473.

MEDLINE; 94306394.

BECKER K.-F., ARKINSON M.J., REICH U., BE SIEWERT J.R., HOEFLER H.;

"E-cadherin gene mutations provide clues carcinomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-16 FROM N.A.

MEDLINE; 94380041.

BUSSEMAKERS M.J., GIROLDI L.A., VAN BOKHOVEN A., SCHALKEN J.A.;

BUSSEMAKERS M.J. regulation of the human E-cadherin gene in human prostate cancer cell lines: characterization of the human E-cadherin gene promoter.";
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MEDLINE; 89031725.

MANSOURI A., SPURR N., GOODFELLOW P.N., KEMLER
"Characterization and chromosomal localization
the human cell adhesion molecule uvomorulin.";
Differentiation 38:67-71(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     VARIANTS GYNECOLOGIC CANCERS THR-617; VAL-711 MEDLINE; 94355983.
RISINGER J.I., BERCHUCK A., KOHLER M.F., BOYD "Mutations of the E-cadherin gene in human gyr mat. Genet. 7:98-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE, 98415721.

BERX G., BECKER K.-F., HOEFLER H.,

"Mitations of the human E-cadherin

"Mitations of the 237(1998).
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KELKER W., WARDA A
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   CARCINOMA
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    PRO-193
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(CDH1) gene.";
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BIRCHMEIER W.,

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EMBL; 213009; CAA78353.1; -
EMBL; 218923; CAA79356.1; -
EMBL; X12790; CAA312779.1; -
EMBL; L34545; CAA3127764.1; -
PIR; S25141; IJHUCE,
PIR; S37654; S37654.
Calcium-binding; F
SIGNAL 1
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CHAIN 155
DOMAIN 155
TRANSSEM 702
REPEAT 155
REPEAT 263
REPEAT 263
REPEAT 376
REPEAT 487
REPEAT 487
REPEAT 487
REPEAT 594
DOMAIN 838
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GUILFORD P., HOPKINS J., HARRAWAY J., MCLEOD M., MCLEOD N.,
HARRAWIRA P., TAITE H., SCOULAR R., MILLER A., REEVE A.E.;
"E-cadherin germline mutations in familial gastric cancer.";
Nature 392:402-405(1998).
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MEDLINE; 97138061.
SOARES P., BERX G., VAN ROY F.,
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MUTA H., NOGUCHI M., KANAI Y., OCHIAI A.,
"E-cadherin gene mutations in signet ring
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MEDLINE; 97197648.
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PFAM; PF01049; Cadherin_C_term; 1.

PROSITE; PS00232; CADHERIN; 3.

Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane;
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MIM; 192090;
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EPITHELIAL-CADHERIN.
EXTRACELLULAR (POTENTIAL).
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-i- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS. THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED 1 NEURONAL RECOGNITION MECHANISM.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"N-cadherin gene maps to human chec-cadherin gene.";
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J. Cell Sci. 102:7-17(1992).
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MIM; 114020;
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01049; Cadherin_C_term;
PS00232; CADHERIN; 3.
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UL-UCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BLASTOMERE-CADHERIN PRECURSOR (B-CADHERIN).
Xenopus laevis (African clawed from)
                                    CADB_XENLA
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Mycoplasma pneumoniae.
Mycoplasma preumoniae.
Bacteria; Firmicutes; Bacillo
Mycoplasmataceae; Mycoplasma
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Nucleic Acids Res. 24:4420-4449(199-1-SIMILARITY: BELONGS TO THE RIBO
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BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.
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SCHNEIDER S.,

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Cell adhesion;
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"Xenopus cadherins: the maternal members of the family.";
Mech. Dev. 47:213-223(1994).
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"Expression of XBcad, a novel cadherin, during oogenesis and early development of Xenopus.";

Mech. Dev. 35:33-42(1991).

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

-I- FUNCTION: CADHERINS ARE CALCIUM THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES.
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TISSUE SPECIFICITY: EXPRESSED IN PITUITARY GLAND, LUNG AND KIDNEY
DEVELOPMENTAL STAGE: DURING OOGENESIS AND EARLY DEVELOPMENT.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                cn 53.5
1 Similarity 50.0
7; Conservative
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01049; Cadherin_C_term; 1.
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W; 147El:
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BLASTOMERE-CADHERIN
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ASN
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AC P33147
DT 01-OCT
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CADO\_XENLA P33147; 01-0CT-1993 01-0CT-1993 01-0CT-1993

(Rel. 27, Created)
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HSSP; P15116; INCH.
PFAM; PF00028; cadherin_C_term; 1
R PFAM; PF01049; Cadherin_C_term; 1
R PROSITE; PS00232; CADHERIN; 3.
PROSITE; PS00232; CADHERIN; Phos
Query Match
Best Local Similarity
Matches 7; Conser
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01-FEB-1991 (Rel.
15-JUL-1998 (Rel.
NEURAL-CADHERIN 1
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P20310;
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XENLA
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-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS
-ITHEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
SORTING OF HETEROGENEOUS CELL TYPES. N-CADHERIN MAY BE INVOLVED
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REPEAT
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- I - SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- I - SIMILARITY: BELONGS TO THE CADHERIN FAMILY.

PIR, JQ0442; IJXLC1.

HSSP; P15116; INCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 90211966. DETRICK R.J., DICK
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodin
                                                                                                                                                                                                                                                                                                                                 REPEAT
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The effects of N-cadherin misexpression on
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PRECURSOR (N-CADHERIN 1)
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17, Last sequence up
36, Last annotation
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                      Score 38;
Pred. No.
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                                           Length 905;
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RESULT 14
YOX1_YEAST
ID YOX1_YEAST
AC P34161;
DT 01-FEB-1994
DT 01-OCT-1996
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Best Local :
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SEQUENCE
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MEDLINE; 91372132.

GINSBERG D., DESIMONE D., GEIGER B.;

"Expression of a novel cadherin (EP-cadherin) in unfertilized eggs
and early Xenopus embryos.";

Development 111:315-325(1991).

Development 111:315-325(1991).

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC
MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE
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HSSP; P15116
                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURAL-CADHERIN 2 PRECURSOR (N-CADHERIN·2).
Xenopus laevis (African clawed frog).
Eŭkaryota, Metazoa; Chordata; Craniata; Ver
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                       PROPEP
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                                                                302
                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             SORTING OF HETEROGENEOUS CELL TYPES, N-CADHERIN NEURONAL RECOGNITION MECHANISM.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
                                                                                                                                                                                                                                                                                                            ; P15116; INCH.
; PF00028; cadherin; 5.
;; PF01049; Cadherin_C_term; 1.
ITE; PS0032; CADHERIN; 3.
adhesion; Glycoprotein; Phosphorylation;
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(Rel:
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
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POTENTIAL.
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Pred. No. 21;
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EXTRACELLULAR (F
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ia; Pipoidea; Pipidae;
                        PRT;
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Xenopodinae;
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                                              Homo sapiens (Human)
Eukaryota; Metazoa; (
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SEQUENCE FROM N-A.

Eutheria;

Primates;

Catarrhini; Chordata;

Craniata;

Vertebrata;

Mammalia

Homo

Hominidae;

TISSUE-LIVER; MEDLINE; 96374830 LIN S.W., CHEN J.O

J.C.,

HSU

L.C.,

HSIEH

C.-L.,

YOSHIDA

ALDH9

OR ALDH7

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Query Match
Best Local S
Matches 7
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EMBL; Z46659; CAA86628.1; -
PIR; S33388; S33388.
HSSP; P06601; 1FJL.
SGD; L0002540; YOX1.
PFAM; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C / AB972;
BADCOCK K. CHURCHER C.,
Submitted (NOV-1994) to t
-i- FUNCTION: IN VITRO,
LEUCINE TRNA GENE.
                                                                                         DHAG_HUMAN
P49189;
01-FEB-1996
U1-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ALDEHYDE DEHYDROGENASE, E3 ISOZYME (EC 1.2.1.3)
AMINOBUTYRALDEHYDE DEHYDROGENASE) (EC 1.2.1.19)
DEHYDROGENASE).
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DNA_BIND
CONFLICT
SEQUENCE
                                                                                                                                                HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeobox gene.";
Chromosoma 102:174-179(1993).
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KAUFMANN E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last annotation update) HOMEOBOX PROTEIN YOX1.
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Pred. No. 8.6;
1; Mismatches
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MEDLINE; 89174735.

A KURYS G., AMBROZIAK W., PIETRUSZKO R.;

A KURYS G., AMBROZIAK W., PIETRUSZKO R.;

T'Human aldehyde dehydrogenase. Purification and characterization of a Third isozyme with low Km for gamma-aminobutyraldehyde.";

L J. Biol. Chem. 264:4715-4721(1989).

-!- FUNCTION: HAS A WIDE SUBSTRATE SPECIFICITY AND A LOW KM FOR 4-AMINOBUTYRALDEHYDE. ITS OPTIMAL PH DEPENDS UPON SUBSTRATE.

C -!- FUNCTION CACTIVITY: ALDEHYDE + NAD(+) + H(2)O = ACID + NADH.

C -!- CATALYTIC ACTIVITY: 4-AMINOBUTANAL + NAD(+) + H(2)O = 4-AMINOBUTANOATE + NADH.

C -!- SUBUNIT: HOMOTETRAMER.

C -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN ADULT LIVER, SKELETAL G. BEALU.

G BRAIN.

C --- AND KIDNEY. LOW LEVELS IN HEART, PANCREAS, LUNG, AND
                                                               Query Match 52.1%;
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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-I- PTM: THE N-TERMINUS IS BLOCKED.
-I- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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MEDLINE; 94094820.
KURYS G., SHAH P.C., KIKONYOGO A., REED D., AMBROZIAK W.,
PIETRUSZKO R.;
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BONFIELD J., BURTON J., CONNELL M., COPER T., COOLSON A
CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P.,
JOHNSTON J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VADGHAN K., WAPERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RELEGALS, CALLAGAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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EMBL; Z80215; CAB02276.1;
SEQUENCE 327 AA; 37139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUTZ D.A., ZHENG J.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF033826; AAB87087.1; -.
PFAM; PF00028; cadherin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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7; Conservative
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145 AA;
  thaliana
                                                                                                                                                               PRELIMINARY;
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15617 MW;
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  (Mouse-ear
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Pred. No.
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Pred. No. 3.9;
3; Mismatches 3
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Guery Match
Best Local S
Matches 8
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Best Local Similarity 42.9
Matches 6; Conservative
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. CALLAN M. C.,
STRAIN-CV. CALLAN M. C.,
STRAIN-CV. CALLAN M. C.,
SOMERVILLE C.R., VENTER J.C.;
SOMERVILLE C.R., VENTER J.C.;
"AFABLIGORS thaliana chromosome II BAC T19C21 genomic sequence.
"AFABLIGORS thaliana chromosome II BAC T19C21 genomic sequence.
"AFABLIGORS thaliana chromosome II BAC T19C21 genomic sequence.
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075309;
01-NOV-1998
01-NOV-1998
01-MAY-1999
                                                                                                                                                                                                                                                             EMBL; AF016272; AAC34255.1; -.
PFAM; PF00028; cadherin; 6.
PROSITE; PS00232; CADDERIN; 2.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat
SEQUENCE 829 AA; 89923 MW; E44B3DBE CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cDNA cloning and chromosomal localization isoforms of Ksp-cadherin."; Genomics 51:445-451(1998). "FOR EXECUTION TYPE I MEMBRANE FEMBL; AP016272; AAC3455.1; "TYPE I MEMBRANE FEMBL; AP016272; AAC34555.1; "TYPE I MEMBRANE FEMBL; AP0162725; AAC34555; AP0162725; AAC34555; AP0162725; AP0162755; AP0162
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MEDLINE; 98389630,
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Eukaryota; Metazoa;
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ARONSON P.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates;
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Similarity 57.: 8; Conservative
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                                                 54.98;
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42.9%;
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Last annotation update)
                                                 Score 39;
Pred. No.
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Mismatches
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     Indels
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Gaps
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Q15855 PRELIMINARY; PRT; 878 AA. Q15855; Q16194; Q13799; Q175855; Q16194; Q13799; Q175855; Q16194; Q17586Lrel. 01, Created) Q1-NOV-1996 (Trembirel. 01, Last sequence update) Q1-MAY-1999 (Trembirel. 10, Last annotation update) QVOMORULIN PRECURSOR (E-CADHERIN) (ARC-1/UVOMORULIN)

160

NSDLRFHILSQAPA NSKIAFKIVSQEPA 15

173

N

Homo sapiens (Human). Eukaryota; Metazoa; Chordata;

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Q28634;
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"Molecular cloning of human E-cadherin suggests a novel
of the cadherin superfamily.";
Biochem. Biophys. Res. Commun. 200:1754-1761(1994).
                      "ISOLEIMANI M., ARONSON P.S.;

"ISOLAtion and cDNA cloning of Ksp-cadherin, a novel kidney-specific member of the cadherin multigene family.";

J. Biol. Chem. 270:17594-17601(1995).

-i. FUNCTION: CADHERINS ARE CALCUMITH THEMSELVES IN A HOMOPHILIC THEY PREFERRITIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SUBCELLULAR LOCATION. TYPE I MEMBRANE PROTEIN.

-i. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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KIDNEY-SPECIFIC CADHERIN PRECURSOR (KSP-CADHERIN).
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BECKER K.F., ATKINSON M.J.,
SIEWERT J.R., HOFLER H.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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-1- SIMILARITY: 1
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"Complementation of divergent m
Gene 175:77-81(1996).
EMBL; X95408; CAA64690.1; -.
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HYPOTHETICAL 16.6 KD PROTEIN.
                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."

DNA Res. 3:109-136(1996).
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MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases. EMBL; X68501; CAA48513.1; -. SEQUENCE 533 AA; 62164 MW; F46E7EF2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SEROTYPE M49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
Bactlus/Clostridium group; Streptococcaceae:
                                                              EMBL; D90899; BAA16672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-PCC6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain
Bacteria; Cyanobacteria; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SEROTYPE M49;
PODBIELSKI A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The group A streptococcal virR49 structural vir regulon genes."; infect. Immun. 63:9-20(1995).
Hypothetical
SEQUENCE: 1
                                                                                                                                                                                                                                              TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 97061201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TABATA S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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MEDLINE; 95105032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1992) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRR49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PODBIELSKI A., FLOSDORFF A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-499 FROM
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8; Conserv
l protein.
138 AA; 16580
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Pred.
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CA436352 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                  KIMURA T.,
NARUO K., OKUMURA S.,
VASUDA M.,
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                                                                                                                                                                                                                                                                                                                                                                           NAKAMURA Y.,
                                                                                                                                regions.";
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Q38172;
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094853;
01-MAY-1999;
01-MAY-1999;
01-MAY-1999;
                                                                                                                                 "A genomic region of lactococcal temperate encoding major virion proteins."; Virology 218:306-315(1996).
EMBL; X84706; CAA59185.1; -. SEQUENCE 273 AA; 28880 MW; E7DA3E03 CRC
                                                                                                                                                                                                                                                                                                             STRAIN-TP901-1, TP936-1, C3-T1;
MEDLINE; 96193742.
JOHNSEN M.G., APPEL K.F., MADSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOTANI H., NOMURA N., OHARA O.;

**prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from the for large proteins in vitro.";

**DNA Res. 5:277-286(1998).*

**EMBL: AB018296: BAA34473.1;

**SEQUENCE 967 AA; 109376 MW; C8749COA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIAA0753
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                                                                                                                                                                                                                                                                                           ARNAU J.
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   Similarity 61.8
8; Conservative
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6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Score 38; DB Pred. No. 18; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tailed phages; Siphoviridae.
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67;
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                                                                                                                                             CRC32
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   4;
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   Indels
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                             RAN MARA SELECTION
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Best Local
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STRAIN-Madrid E;

ANDERSSON S.G.E.;

Submitted (NOV-1998) to the EMBI
EMBL; Y11780; CAA72468.1; -
EMBL; AJ235270; CAA14683.1; -
EFAM; PF01259; SAICAR_SYNT; 1.
SEQUENCE 236 AA; 27310 MW; 1
SEQUENCE ...
STRAIN-MADRID E;
MEDLINE; 99039499.
ANDERSSON S.G.E., ZOMORODIPOUR A., ANI
SICHERITZ-PONTEN T., ALSMARK U.C.M.,
SICHERITZ-PONTEN T., ALSMARK U.C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997
01-JUL-1997
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      005946;
                                                                                                                                                                                                                                                                                                                                  Q9ZCYO PRELIMINARY;
Q9ZCYO;
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic rearrangements during evolution of intracellular parasite Rickettsia prowazekii analysis of 52015 bp nucleotide sequence."; Microbiology 143:2783-2795(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia prowazekii.
Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINCCARBOXAMIDE SYNTHASE
                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                            Rickettsia
                                                                                                                                                                                                                                                                     SODIUM/PANTOTHENATE
                                                                                                                                                                                                                                                                                           01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondria.
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ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O., SICHERITZ-PONTEN T., ALSWARK U.C.M., PODOWSKI R.M., ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-Madrid E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-MADRID E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PURC OR RP220
                                                                                                                                                                                 Rickettsiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence
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5; Conservative
                                                                                                                                                                                 Proteobacteria; alp
nceae; Rickettsieae;
                                                                                                                                                                                                                        prowazekii.
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(Tremblrel. 10, Last ann
)THENATE SYMPORTER (PANF)
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eae; Rickettsia.
                                                                                                                                                                                 alpha subdivision;
eae; Rickettsia.
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Last annotation update)
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                             M., PODOWSKI R.M., AND C.G.;
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24;
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STRAIN-MADRID E;
ANDERSSON S.G.E.;
ANDERSSON S.G.E.;
Submitted (NOV-1998) to the
EMBL; AJ235272; CAA15019.1;
SEQUENCE 461 AA; 51674 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                                                                     CHAILLECT CONTROL 13 and mouse chromosome 14.; localized on human chromosome 13 and mouse chromosome 14.; localized on human chromosome 13 and mouse chromosome 14.; localized on human chromosome 15. If I was a suppose 15. If I was a suppose 15. If I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15. I was a suppose 15
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[2]
                                                                                                                                                                                                                                                                                                                                 "Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Genome :
Mitochondria
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 99005535
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTOCADHERIN.
  646
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                                        NSKIAFKIVSQEP
NGELAFELQQEP
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                                                                                 Similarity 46.
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  658
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46.2%;
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LIU
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46.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                      auto-limined disease

Claim 1: Page 38; 58pp: English.

Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-myslin basic protein (MBP) polypeptide which is capable of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA-DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive disease and which binds to the polypeptide to activate autoreactive and implicated as a self epitope in pemphigus vulgaris. Peptides derived from the human desmoglein 3 protein are described in W04841-47.

Sequence 15 AA;
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Best Local Similarity
Matches 15; Conser
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Best Local :
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        17-JUN-1997 (first entry)
Pemphigus foliaceus antigen-IgG constant region fusion protein.
Pemphigus foliaceus; autoantibody; constant region; IgG;
extracellular region; antigen; hinge portion; skin;
dermatitis herpetiformis; fusion protein; detection; ss.
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Sequence
                                                                                                         W15489 standard; Protein; 778 AA
 Chimeric
                                                                                            W15489;
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Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens useful in disease treatment, and method for identification of other self and non-self antigens implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1996.
07-MAR-1996; U03182.
07-MAR-1995; US-400796.
(HARD) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Self epitope of desmoglein 3, implicated in autoimmune disease. Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strominger JL,
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WO9627387-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herpes simplex virus; adenovirus; phosphomannomutase;
human papillomavirus; Epstein-Barr virus; DNA polymerase;
influenza; haemagglutinin; reovirus; sigma protein.
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614 AA;
 Homo
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Pred. No.
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Pred. No.
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TOKITYRISGYGID

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Query Match Best Local S Matches 6

Similarity 42. 6; Conservative

56.8%;

Score 42; DB Pred. No. 6; 4; Mismatches

1; L 4;

Length 551

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pemphigus foliaceus antigen-IgG constant region fusion protein - linked retrough the hinge region used to treat pemphigus foliaceus claim 1; Page 10-12; 17pp; Japanese.

This sequence represents a fused protein recognised by pemphigus foliaceus patient autoantibody which comprises the constant region cof IgG linked to the extracellular region of pemphigus foliaceus is a chronic, generalised, vesicular and scaling skin eruption similar to dermatitis herpetiformis. The pemphigus foliaceus antigen fusion protein is useful to treat pemphigus foliaceus antigen is cespecially administered through an adsorbent upon which the fusion protein is immunobilised via a carrier. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful in immunodiagnosis. The fusion protein is also useful for detecting pemphigus foliaceus antibodies which is useful in immunodiagnosis. The fusion protein is also
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Best Local Similarity
                                                                                           Kraus Jr.
WPI; 95-131185/17.
N-PSDB; Q874400.
Purified DNA encoding human cystathionine beta-synthase -
Purified DNA encoding human cystathionine beta-synthase, used for
for producing human cystathionine beta-synthase, used for treating homocystinuria Claim 7; Fig la-c, 45pp; English.
The amino acid sequence shown in R71376 is the human cystathionine beta-synthase (CBS). Human CBS can be used to treat patients with homocystinuria and the cDNA sequence, Q87430, from which it is derived is also useful for screening CBS deficient patients for mutations in the CBS gene.

Sequence 551 AA;
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                                                                                                                                                                                                                                                                                                         21-NOV-1995 (first entry)
Human cystathionine beta-synthase
Cystathionine; beta synthase; hum
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25-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                             R71376 standard;
R71376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in immunodiagnosis. Sequence 778 AA;
                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                               12-SEP-1994;
13-SEP-1993;
                                                                                                                                                                                                                                                               23-MAR-1995.
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12-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 ANQOVTYRISGYGID 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATQKITYBISGVGID
                                                                                                                                                                                                              UNIV
                                                                                                                                                                                                            ; U10203.
; US-120960.
/ COLORADO.
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Copyright (c) 1993 - 1998 Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      than or equal to the
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6.922 Million cell updates/
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E. camis p30-6 pro
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Sequence of human
Human E-cadherin p
Full length human
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Human glaucoma ass
Human TIGR protein
Trabecular meshwor
Trabecular meshwor
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Best Local S
Matches 15
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J08188540-A.

23-JUL-1996.
30-JUN-1994; JP-173391.
(NISH/) NISHUKAWA T.
WPI; 96-388562/39.
Fused protein recognised by pemphigus vulgaris auto:antibody - useful to treat and diagnose pemphis vulgaris
Claim 1; Page 7-9; 9pp; Japanese.
W07908 represents the human pemphigus vulgaris (PV) antigen extracellular region. The PV antigen is produced in patients with pemphis vulgaris resulting in autoimmune disease. PV is a rare relapsing disease causing superall, intra-epidermal bullae (vesicles) of the skin and mucuous membranes, which is fatal if untreated. The PV antigen was fused to a human IgG1 hinge region and the resulting fusion protein is useful to treat or diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding pemphiqus vulgaris antigen - useful in proteins for diagnostic and therapeutic uses Disclosure; Fig 7; 50pp; English.

This sequence is the pemphigus vulgaris 130kD antigen. The protein and its encoding DNA may be used in the diagnosis and treatment of pemphigus vulgaris. It is thought that the antigen may be a cell adhesion molecule.

Sequence 999 AA;
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14-JUN-1993
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Autoantibody; immunoglobulin G; IgGl; fusion protein; diagnosis;
treatment; pemphigus vulgaris; PV; bulla; blister; skin disease;
                                                                                                                                                                                                                                                                                                                                                                                        dermatology.
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Pemphigus vulgaris; skin disease; autoantibodies;
keratinocyte cell surface antigen; glycoprotein;
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W07908;
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(USSH) US DEPT HEALTH &
Amagai M, Klaus-kovtun v
WPI; 93-067436/08.
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15-DEC-1992.
27-NOV-1991, 798918.
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Pred. No. 1.3e-05;
Mismatches 0;
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Number of hits that pass the threshold

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Pred. No. score

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Scoring table: Sequence: Title Perfect score:

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Job time: 1681 sec
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WHY; 99-181045/15.

RN PSDB; X34112.

RY-SCOBE; X34112.

Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression

Claim 32; Fig 18F; 309pp; French.

Sequences Y04742-Y05000 and Y07201-y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.

Sequence 390 AA;
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Best Local Si
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Best Local Similarity
Matches 6; Conserv
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14-AUG-1998; FO1813.
11-SEP-1997; FR-011325.
14-AUG-1997; FR-010404.
(INSP) INST PASTEUR.
Gicquel B, Lim EM, Pelicic V, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1999 (first entry)
06-JUL-1999 (first entry)
Mycobacterium species protein sequence 18F.
Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
Mycobacterium sp.
Mycobacterium sp.
Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the E2 initiation codon. The E2 and E3 genes have been cloned and can be used for the recombinant production of BCV polypeptides, using e.g. Spodoptera frugiperda Sf9 insect cells as host cells. Glycosylated and non-glycosylated recombinant E2 and E3 (see W31707) are useful as components of vaccines directed toward preventing BCV infection, or reducing the severiof BCV infection, in bovine populations.
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Y04860;
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Pred. No. 35;
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RESULT
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Best Local
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10-AUG-1999; CA0252.
22-AUG-1989; US-397689.
(VETE-) VETERINARY INFECTIO.
Parker MD, Cox GJ, Babiuk LA;
WPI: 91-887247/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E3 useful as vaccine component Disclosure; Fig 3 (1-6); 70pp; English. E2 ar E2 protein is one of the four proteins (N. E1, E2 ar BCV. The E2 and E3 polypeptides, or fragments of th subunit antigens in vaccines for protection against BCV, without risk of infection.

Sequence 1363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               incorporated with its coding gene.

Claim 2; Fig 1f; 20pp; Japanese.

DNA encoding the protein can be inserted into an expression vector for the prodon. of MG-1 polypeptide which elivits in intigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal bacterial enzyme sequence.
                                         Segment of desmosomal cadherin, desmoglein Dsg2.
Desmosomal cadherin; desmoglein; Dsg2; cell; surface; epithelial; carcinoma; desmosome; antibody; epitope; diagnosis; detection; micrometastasis; separation; enrichment; targetted delivery;
                                                                                                                                                                 W13009 standard; protein; W13009;
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Bovine Coronavirus; BCV; E2; E3; vac
Bovine coronavirus - Quebec isolate.
Bovine coronavirus - Quebec isolate.
Location/Qualifiers
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                        metastatic.
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7; Conserv
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Pred. No. 1.46
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1.4e+02;
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f these, a
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosomes, useful for diagnosis and treatment of carcinoma micrometastases of claim 7; Page 5; Bpp; German.

The present sequence is a segment of the desmosomal cadherin (DC), desmoglain Bg2, which is exposed on the surface of epithelial or carcinoma cells and not bound to desmosomes. An antibody (Ab) of directed against epitopes of the present sequence can be used to diagnose, i.e. to detect carcinoma cells, especially micrometastases, not bound to desmosomes, to separate, enrich or detect living or fixed carcinoma cells by cell sorting methods and cas a therapeutic to deliver agents, e.g. other Ab or toxins, to metastatic carcinoma, and detects parts of DC that are not accessible in desmosome bound cells, as in normal tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE19531033-A1.
27-FEB-1997.
23-AUG-1995; D31033.
23-AUG-1995; DE-031033.
(PROG-) PROGEN BIOTECHNIK GMBH.
Franke WW., Schaefer S;
                                                                                                                                                                                                                              22-AUG-1989; 397689.
19-DEC-1991; US-811422.
22-AUG-1989; US-397689.
18-OCT-1991; US-779500.
22-DEC-1993; US-171763.
Vaccines against bovine coronavirus - containing recombinant bovoronavirus polypeptide(s)
Claim 13; Fig 3; S2pp; English.
This polypeptide comprises the E2 protein, also designated peplomer protein or S (Spike), of bovine coronavirus (BCV). It has a moll.wt. of 150 kDa exclusive of glycosylation and contains 21 potential N-linked glycosylation sites. The amino acid sequence was deduced from an clone E2 cDNA (see T89387). The E2 gene in plasmid pri8E2 (E. coll JM105) is deposited as ATCC 68041. The BCV E3 gene (see T89388) is immediately 5' of the E2 gene on the viral genome and terminates 14 nucleotides upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine coronavita
BCV; E2 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Franke WW, Schaef WPI; 97-146518/14.
                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W31706
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                                                                                                                                                                    (VETE-) VETERINARY INFECTIOUS Babbuk LA, COX GJ, Parker MD; WPI, 97-488823/45.
N-PSDB; T89387.
                                                                                                                                                                                                                                                                                                                         JS5672350-A.
                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                               coronavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560
                                                                                                                                                                                                                                                                                                                                       /label= Mat_protein
1306. .1338
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                   /label- Sig_peptide
18. .1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rst entry)
us E2 (S) protein.
peplomer protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                      recombinant bovine
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Best Local S
Matches 8
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(TIGR*) protein, that is highly induced by glucocorticoids in the
endothellal lining of the human trabecular meshwork (HTM). The
sequence was deduced from an isolated cDNA clone (see V33484).
Studies of the recombinant protein suggest (1) that the 55 kDa
protein exists both in cells and in the medium, (2) that it
undergoes oligomerisation, (3) phosphorylation, (4) glycosylation,
(5) that it is susceptible to metalloprotease, (6) that it
exhibits high affinity binding to extracellular matrix and HTM
cells, (7) that it exhibits progressive inductions with time in
both cell and organ cultures, and (8) that it exhibits high
expression in the HTM of glaucomatous patients as compared to
normal patients. TIFR* cDNA, the protein itself, molecules that
bind it, and nucleic acid molecules that encode it, provide
improved methods and reagents for diagnosing glaucoma and related
disorders, such as cardiovascular and immunological diseases that
affect expression of TIGR*. A claimed method of diagnosing glaucoma
involves determining if the amount of TIGR* present in the HTM
exceeds the amount found in an individual not predisposed to the
                        Claim: 1; Column 25-28; 22pp; English.
Claim: 1; Column 25-28; 22pp; English.
This sequence represents the human Trabecular meshwork induced glucocorticoid response (TIGR) protein. The TIGR protein is a sportein specifically bound by the antibody of the invention. The antibody, especially in labelled form, can be used in the diagrigation of the protein in the transcript of the eye. Using the antibody, glaucoma is detected resembly of the eye. Using the antibody, glaucoma is detected resembly.
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                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
Huang W, Nguyen TD, Polansky JR;
WPI; 99-069807/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New protein induced in trabecular meshwork cells by glucocorticoids - useful in the diagnosis of glaucoma and related diseases Claim 1; Fig 1A-c; 53pp; English:
This is the amino acid sequence of a new human 55 kDa protein,
                                                                                                                                                                                                                                                     14-MAY-1996; 645900.
14-MAY-1996; US-645900.
03-NOV-1994; US-336235.
20-OCT-1995; US-546568
                                                                                                                                                                                                                                                                                                                                                                                                  Trabecular meshwork induced glucocorticoid response protein.
TIGR protein; trabecular meshwork induced glucocorticoid res
               accurately.
                                                                                                                                                               glaucoma
                                                                                                                                                                               Antibody to
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    secretory protein;
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G W, Nguyen TD
98-542701/46.
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8; Conservative
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                                                                                                                                                                                trabecular meshwork
                                                                                                                                                                                                                                                                                                                                                                                 antibody; glaucoma;
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57.1%;
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Pred.
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ed. No. 20;
Mismatches
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Query Match Best Local Similarity

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39; 20;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT New isolated glaucoma-associated nucleic acids - which encode probably of glaucoma-associated nucleic acids - which encode processor develop products for diagnosing glaucoma-related diseases (laim 1; Fig 1; 22p; English.)

CC The secretory protein is designated TiGR (Trabecular Meshwork Induced CC The secretory protein is designated TiGR (Trabecular Meshwork Induced CC Glucocorticoids in the endothelial lining cells of the human trabecular meshwork. The TIGR polynucleotides and proteins can be used as markers (for the diagnosis of glaucoma, primary open angle glaucoma (POAG), CC pigmentary glaucoma, and low tension glaucoma and their related diseases. They can also be used to diagnose or protect an individual's sensitivity to elevated intraocular pressure upon administration of steroids such as glucocorticoids or corticosteroids. These products can also be used for diagnosing other diseases or conditions that affect the expression or activity of the protein. The products can also be sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conser
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                                                                                   24-APR-1990.
02-JUN-1989; 136343.
02-JUN-1989; JP-136343.
(JAPG) Nippon Zeon KK, ((JAPG) 90-169109/22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1997; 882238.
17-MAY-1996; US-649432.
03-NOV-1994; US-336235.
20-CCT-1995; US-546568.
25-JUN-1997; US-882238.
                                                                                                                                                                                                                                                                                                                                                     R0644
                             N-PSDB; Q05653
Diagnostic and
                                                                                                                                                                                                                                                                                      MG-6 antigen
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Human; trabecular meshwork induced glucocorticoid response protein;
TIGR; glaucoma; primary open angle glaucoma; POAG; pigmentary glaucoma;
low tension glaucoma; intraocular pressure; steroid; corticosteroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W89391;
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N-PSDB; V81910
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US5854415-A.
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and vaccine of the
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57.1%;
  for poultry mycoplasma serum disease and recombinant vector
                                                                                                                 (SHIO) Shionogi KK
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Pred. No.
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09-JAN-1998. U00468.
26-SEP-1997. US-938669.
28-JAN-1997. US-931144.
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Chen H, Chen P, Nguyen TD, F
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07-NOV-1997; U20702.
21-MAR-1997; US-822999.
08-NOV-1996; US-748479.
30-JAN-1997; US-791347.
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WPI; 98-286947/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduce the severity of the condition. Derivatives of GLCIA gene can be used to detect lesions of the GLCIA gene which are indicative of glaucoms or predisposition to glaucoma.

Sequence 504 AA;
Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma Claim 48; Fig 8; 105pp; English.

This sequence represents a novel human trabecular meshwork induced glucocorticoid response protein (TIGR) which is used in a method for
                                                                                                                                                                                                                                                                                                                                                                                                            Human TIGR protein.
TIGR; trabecular meshwork induced glucocorticoid response protein; diagnosis; glaucoma; polymorphism; steroid sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products to determine whether a subject has, or is at risk of, developing glaucoma, and for treating or preventing glaucoma developing glaucoma, and for treating or preventing glaucoma Disclosure; Pages 92-94; 116pp; English.

This represents a human GLC1A protein sequence. The human GLC1A gene is associated with juvenile open angle glaucoma (JOAG). The gene can be us for the development of assays for identifying molecules that modulate (agonists or antagonists) the bloactivity of a functional or mutant gen or protein. Modulators may be an antibody, protein, peptide or peptidomimetic or a nucleic acid, e.g. antisense sequence, ribozyme or triple helix forming nucleic acid. These molecules can be administered as a subject of the forming nucleic acid.
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New isolated gene associated with glaucoma
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27-OCT-1998 (first entry)
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treatment; mutant; juvenile open angle glaucoma;
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!rabecular meshwork induced glucocorticoid response*; TIGR*;
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